

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 15:14:51 ; Search time 21 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILLGLLLGLHGLTVDTYGR.....LDDTVPLDYEFPLATEGKSVC 399

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	178.5	8.5	299	2	S56749	junctional adhesio
2	178	8.5	7962	2	I38346	elastic titin - hu
3	170	8.1	365	2	JC7780	coxsackie- and ade
4	144.5	6.9	1033	2	S19247	cell adhesion prot
5	143.5	6.8	1052	2	B49120	protein-tyrosine k
6	139.5	6.6	3707	2	S18252	heparan sulfate pr
7	139	6.6	1106	1	PFHUGB	platelet-derived g
8	138.5	6.6	1323	2	PN0568	connectin 3B - chi
9	138.5	6.6	4162	2	T42633	connectin/citin -
10	136	6.5	584	2	T08678	hypothetical prote
11	133.5	6.4	5175	2	T20992	hypothetical prote
12	133.5	6.4	5198	2	T43290	hemiscentin precurs
13	132.5	6.3	765	2	C42632	cell adhesion mole
14	132.5	6.3	812	2	B42632	cell adhesion mole
15	132.5	6.3	932	2	A42632	cell adhesion mole
16	132.5	6.3	1272	2	S26180	neurofascin - chic
17	132	6.3	1896	2	T08851	Down syndrome cell
18	131	6.2	4391	2	A38096	perlecan precursor
19	129.5	6.2	1040	2	A34695	axonal glycoprotei
20	129.5	6.2	3375	2	T19821	hypothetical prote
21	129.5	6.2	6658	2	T13931	projectin - fruit
22	129	6.1	309	2	I49522	gene B7-2 protein
23	129	6.1	1427	2	I51669	tumor suppressor -
24	129	6.1	1906	1	S68235	myosin-light-chain
25	128.5	6.1	338	2	JC5519	50K glycoprotein p
26	127	6.1	725	1	IJMSNG	neural cell adhesi
27	127	6.1	1115	1	IJMSNL	neural cell adhesi
28	125.5	6.0	1259	2	A43425	Bravo/Nr-CAM cell
29	125	6.0	351	2	JH0396	biliary glycoprote

30	124	5.9	853	1	IJBONC
31	124	5.9	1011	2	T13669
32	124	5.9	1344	2	T14316
33	123.5	5.9	458	1	WMMSR1
34	123.5	5.9	521	2	JC1508
35	123.5	5.9	1091	1	IJCHNL
36	123	5.9	464	2	C30127
37	123	5.9	467	1	HIMSP3
38	123	5.9	526	1	A32164
39	123	5.9	1694	2	S50065
40	122.5	5.8	738	2	A40096
41	122.5	5.8	761	1	IJHUNG
42	122.5	5.8	1268	1	A39640
43	122	5.8	1036	2	S22383
44	121	5.8	538	2	JC2457
45	121	5.8	816	2	A49151
46	120.5	5.7	458	2	JC1509
47	120	5.7	333	2	A31923
48	119.5	5.7	417	2	JH0394
49	119.5	5.7	483	2	T17346
50	119.5	5.7	547	2	B45808
51	119.5	5.7	725	2	JE0100
52	119.5	5.7	917	2	I48950
53	119	5.7	806	1	TVHUF3
54	119	5.7	1091	2	A58532
55	119	5.7	26926	1	I38344
56	118.5	5.6	458	2	S68177
57	118.5	5.6	458	2	S23369
58	118.5	5.6	519	2	A44783
59	118	5.6	547	1	S28904
60	118	5.6	1338	2	S09982
61	117.5	5.6	338	2	JC4776
62	117.5	5.6	344	2	A27681
63	117.5	5.6	1092	1	JN0635
64	117.5	5.6	1239	1	A32579
65	117	5.6	739	2	JS0675
66	117	5.6	858	1	IJRTNC
67	117	5.6	1447	2	A54100
68	116.5	5.6	478	2	I53960
69	116.5	5.6	806	2	A35963
70	116.5	5.6	1040	2	A49356
71	116.5	5.6	1051	2	A39712
72	116	5.5	344	2	I56551
73	115.5	5.5	292	2	S03421
74	115.5	5.5	293	2	A40131
75	115.5	5.5	725	2	JE0099
76	115.5	5.5	1257	1	A41060
77	115	5.5	1209	2	T42718
78	114.5	5.5	521	2	S34337
79	114.5	5.5	530	2	A53437
80	114.5	5.5	538	2	I68093
81	114.5	5.5	639	2	I61719
82	114.5	5.5	1088	1	IJXLNL
83	114.5	5.5	1173	2	T25893
84	114	5.4	499	2	S33766
85	114	5.4	544	2	JC5018
86	114	5.4	602	2	A45769
87	114	5.4	773	1	QRRBG
88	113.5	5.4	417	2	A44194
89	113	5.4	1277	2	T30532
90	112.5	5.4	321	2	JH0395
91	112.5	5.4	345	2	JC4025
92	112.5	5.4	462	2	I38404
93	112.5	5.4	518	2	JC4024
94	112.5	5.4	640	2	A43273
95	112.5	5.4	1259	2	S36126
96	112.5	5.4	2029	1	TDFFLK
97	112	5.3	946	1	A47299
98	112	5.3	976	2	T29583
99	112	5.3	1273	2	T42405
100	112	5.3	1530	2	AH1396
101	111.5	5.3	1070	2	JC4593
102	111	5.3	6642	2	T29757

neural cell adhesi
neuromusculin - fr
rig-1 protein - mo
biliary glycoprote
biliary glycoprote
neural cell adhesi
transmembrane carc
poliovirus recepto
biliary glycoprote
sialoadhesin - mou
platelet-endotheli
neural cell adhesi
neural cell adhesi
axonin 1 precursor
vascular cell adhe
fibroblast growth
biliary glycoprote
amalgam protein pr
biliary glycoprote
hypothetical prote
B-lymphocyte antig
neural cell adhesi
telencephalin prec
fibroblast growth
glial cell membran
titin, cardiac mus
C-CAM2a protein is
ecto-ATPase precur
intercellular adhe
protein-tyrosine k
limbic-system-asso
nonspecific cross-
neural cell adhesi
neuroglial - fruit
vascular cell adhe
neural cell adhesi
tumor suppressor p
PRR2 alpha - human
protein-tyrosine k
transient axonal g
kinase-like protei
neurotrophin - rat
T-cell receptor de
neural cell adhesi
neural cell adhesi
probable neural ce
biliary glycoprote
poliovirus recepto
PRR2 delta - human
neu differentiation
neural cell adhesi
hypothetical prote
platelet-derived g
intercellular adhe
acetylcholine rece
secretory componen
poliovirus recepto
neural cell adhesi
biliary glycoprote
opioid-binding cel
neu differentiation
poliovirus recepto
herregulin precurs
neural cell adhesi
protein-tyrosine-p
ror-related recept
hypothetical prote
bax-3 protein - Ca
peptidoglycan anch
protein-tyrosine k
protein UNC-89 - C

103	110.5	5.3	349	2	A34815	carcinoembryonic a
104	110	5.2	417	1	RWHUPA	poliovirus recepto
105	110	5.2	626	1	BNRT3	myelin-associated
106	110	5.2	1880	2	T18531	tractin - medicina
107	110	5.2	2295	2	C88369	protein unc-52 [im
108	109.5	5.2	338	2	JC1238	opioid-binding pro
109	109.5	5.2	345	2	JC1239	opioid-binding pro
110	109.5	5.2	526	2	S70587	butyrophilin precu
111	109.5	5.2	800	2	A48991	heparin-binding gr
112	109.5	5.2	801	2	I55363	fibroblast growth
113	109.5	5.2	1336	2	I60598	Fit-1 tyrosine kin
114	109	5.2	646	2	I38049	cell surface glyco
115	108.5	5.2	345	2	S03199	colon carcinoma-as
116	108.5	5.2	416	2	A54017	myelin-associated
117	108.5	5.2	637	2	B33785	fibroblast growth
118	108.5	5.2	819	1	TVCHFG	connectin/tilin -
119	108.5	5.2	1021	2	T42634	hypothetical prote
120	108.5	5.2	1328	2	T23007	butyrophilin - bov
121	108	5.1	526	2	A37821	neu differentiation
122	108	5.1	636	2	I61718	platelet-derived g
123	108	5.1	1098	1	PFGMRB	duct1 protein - mo
124	108	5.1	1612	2	T30805	fibroblast growth
125	107.5	5.1	800	1	TVHU2F	fibroblast growth
126	107.5	5.1	818	2	JC4058	fibroblast growth
127	107.5	5.1	829	2	JC4583	fibroblast growth
128	106.5	5.1	354	1	S42938	proteoglycan link
129	106.5	5.1	662	2	C40862	heparin-binding gr
130	106.5	5.1	822	1	TVHUEG	fibroblast growth
131	106.5	5.1	1227	2	T23004	hypothetical prote
132	106.5	5.1	1232	2	T43027	neural cell adhesi
133	106	5.1	582	1	BNRT3S	myelin-associated
134	106	5.1	797	2	S38579	fibroblast growth
135	106	5.1	919	2	T32541	unc-5 protein - Ca
136	106	5.1	947	1	B44294	unc-5 protein, lon
137	106	5.1	1040	2	A57638	receptor tyrosine
138	106	5.1	1103	2	T22889	hypothetical prote
139	105.5	5.0	423	2	T29549	hypothetical prote
140	105.5	5.0	729	2	A56795	fibroblast growth
141	105.5	5.0	733	2	I49293	fibroblast growth
142	105.5	5.0	822	2	I49289	fibroblast growth
143	105.5	5.0	822	2	S29840	fibroblast growth
144	105.5	5.0	940	2	A40985	projectin - fruit
145	105.5	5.0	1256	2	T03096	CDO protein - rat
146	105	5.0	862	2	I49583	differentiation an
147	104.5	5.0	268	2	T23555	hypothetical prote
148	104.5	5.0	392	2	B44194	poliovirus recepto
149	104.5	5.0	599	2	T16774	hypothetical prote
150	104.5	5.0	1021	2	I39207	leukocyte surface
151	104.5	5.0	1184	2	T09484	cartilage intermed
152	104.5	5.0	2222	2	T13924	sdk protein - fruit
153	104.5	5.0	2783	2	T34416	hypothetical prote
154	104	5.0	299	1	AHRB	Ig alpha chain C r
155	104	5.0	338	2	S09276	Ig alpha chain C r
156	104	5.0	637	2	C43273	heregulin precursor
157	104	5.0	662	2	I61722	neu differentiation
158	104	5.0	882	2	I38912	receptor tyrosine
159	104	5.0	1356	2	JC1402	protein-tyrosine k
160	103.5	4.9	628	2	I38000	lutheran blood gro
161	103.5	4.9	647	2	A35648	B-cell adhesion pr
162	103.5	4.9	822	1	TYMSFG	fibroblast growth
163	103.5	4.9	824	2	S36439	fibroblast growth
164	103.5	4.9	832	2	JH0393	fibroblast growth
165	103.5	4.9	847	2	JH0371	B-cell adhesion pr
166	103.5	4.9	6831	2	A88852	protein unc-22 [im
167	103.5	4.9	6839	2	S57242	twitchin [similari
168	103.5	4.9	7160	2	T27935	hypothetical prote
169	103	4.9	811	2	A41054	fasciclin II, tran
170	103	4.9	873	2	B41054	fasciclin II, PI-II
171	103	4.9	1742	2	S24600	projectin - fruit
172	102.5	4.9	318	2	F72171	K9R protein - vari
173	102.5	4.9	1176	2	JN0583	myosin-light-chain
174	102.5	4.9	1651	2	T14160	transmembrane rece
175	102	4.9	626	1	A61084	myelin-associated
176	102	4.9	702	2	A36319	carcinoembryonic a
177	102	4.9	871	1	I48696	protein-tyrosine k
178	102	4.9	881	1	I48697	protein-tyrosine k
179	101.5	4.8	392	1	RWHUPD	poliovirus recepto
180	101.5	4.8	413	2	S65948	hemolin - cecropia
181	101.5	4.8	413	2	A37778	hemolin precursor
182	101.5	4.8	898	2	A40114	fasciclin II precu
183	101.5	4.8	1260	1	S05479	neural cell adhesi
184	101.5	4.8	1526	2	T13823	frazzled gene prot
185	101	4.8	267	2	A38442	probable tumor sup
186	101	4.8	584	2	I50419	Schwann cell myeli
187	101	4.8	620	2	JH0593	fibroblast growth
188	101	4.8	713	2	I50128	CD22 homolog/B lym
189	101	4.8	868	1	A46512	protein-tyrosine k
190	101	4.8	890	1	A53743	frazzled gene prot
191	101	4.8	1375	2	T13822	hypothetical prote
192	100.5	4.8	288	2	T24824	proteoglycan link
193	100.5	4.8	355	1	LKCH	proteoglycan link
194	100.5	4.8	408	1	LKRT2	meprin A (EC 3.4.2
195	100.5	4.8	700	1	HYHUMB	protein-tyrosine k
196	100.5	4.8	790	2	A39627	fibroblast growth
197	100.5	4.8	802	1	TVHUF4	B7-2 antigen - hum
198	100	4.8	329	1	A48754	proteoglycan link
199	100	4.8	354	1	LKHU	brain-derived neur
200	100	4.8	520	1	S44099	brain-derived neur
201	100	4.8	818	1	S44098	CD4 precursor - ra
202	99.5	4.7	459	2	A46254	brain-derived neur
203	99.5	4.7	476	1	A35104	brain-derived neur
204	99.5	4.7	821	1	S06943	BIG-1 protein - ra
205	99.5	4.7	1028	2	I58164	vascular endotheli
206	99.5	4.7	1379	2	JC4954	hypothetical prote
207	99.5	4.7	1666	2	A48594	FP31 protein - fow
208	99.5	4.7	2025	2	T21588	31R protein - vari
209	99	4.7	275	2	H35216	pregnancy-specific
210	99	4.7	313	2	JQ1862	T-cell surface gly
211	99	4.7	424	2	B36109	heregulin, splice
212	99	4.7	458	1	RWHUT4	hypothetical prote
213	99	4.7	645	2	B43273	fibroblast growth
214	99	4.7	773	2	T46283	protein-tyrosine k
215	99	4.7	812	1	A36477	embryonic receptor
216	99	4.7	1367	2	A41228	receptor tyrosine
217	98.5	4.7	1330	2	S49010	Ig heavy chain pre
218	98.5	4.7	1333	2	I78875	protein-tyrosine k
219	98	4.7	380	2	S12839	protein-tyrosine k
220	98	4.7	880	1	JC4166	protein-tyrosine k
221	98	4.7	880	2	B53743	protein-tyrosine-p
222	98	4.7	1499	2	I50212	T-cell receptor de
223	97.5	4.6	144	2	S36308	proteoglycan link
224	97.5	4.6	354	1	S04243	brain-derived neur
225	97.5	4.6	477	1	I73631	B-CAM protein - hu
226	97.5	4.6	588	2	I37202	fibroblast growth
227	97.5	4.6	729	2	A49120	irregular chiasm C
228	97.5	4.6	764	2	A49448	brain-derived neur
229	97.5	4.6	822	1	A56853	protein-tyrosine k
230	97.5	4.6	876	2	I49152	cell surface prote
231	97.5	4.6	1348	2	AH1115	neogenin - chicken
232	97.5	4.6	1443	2	I50600	T-cell receptor al
233	97	4.6	116	2	D24891	hypothetical prote
234	97	4.6	307	2	S55596	alpha-1-B-glycopro
235	97	4.6	474	1	OMHUIB	vascular cell adhe
236	97	4.6	739	2	A41288	DNA helicase/prima
237	97	4.6	751	2	T42597	protein-tyrosine k
238	97	4.6	824	2	S24108	c-mex tyrosine kin
239	97	4.6	994	2	I49276	plasmacytoma-assoc
240	97	4.6	1028	2	A53449	myosin-II-light-chain
241	97	4.6	1147	2	A59307	cardiac myosin-bin
242	97	4.6	1274	2	S55050	hypothetical prote
243	97	4.6	1321	2	T00382	peroxidasin - frui
244	97	4.6	1535	2	S46224	T-cell receptor de
245	96.5	4.6	288	2	A31326	hypothetical prote
246	96.5	4.6	313	2	T28598	KIAA0992 protein -
247	96.5	4.6	772	2	T13078	hyalin - sea urchi
248	96.5	4.6	1200	2	T17404	

249	96.5	4.6	2013	2	AD1129	probable peptidogl
250	96	4.6	243	2	S25755	Ig lambda chain -
251	96	4.6	364	2	A30521	myeloid cell surfa
252	96	4.6	407	2	C82428	glucose-1-phosphat
253	96	4.6	739	2	JN0581	vascular cell adhe
254	96	4.6	1262	1	B48758	protein-tyrosine-p
255	96	4.6	1483	2	C97012	probably celluloso
256	96	4.6	1496	1	A48758	protein-tyrosine-p
257	96	4.6	6805	2	S20901	titin - rabbit (fr
258	95.5	4.6	243	2	A53244	leukocyte antigen
259	95.5	4.6	328	2	S30444	ST2 protein - huma
260	95.5	4.6	887	2	AD2009	hypothetical prote
261	95.5	4.6	1132	2	A35089	myosin-binding pro
262	95	4.5	137	2	I46628	rearranged T-cell
263	95	4.5	814	1	A39752	fibroblast growth
264	95	4.5	1450	2	A44027	165K myofibrillar
265	95	4.5	1501	2	I58148	protein-tyrosine-p
266	95	4.5	1863	2	S46217	protein-tyrosine-p
267	95	4.5	1907	2	S50893	plexin A - fruit f
268	95	4.5	1945	2	T13937	T-cell receptor de
269	94.5	4.5	135	2	S36314	hemagglutinin prec
270	94.5	4.5	315	1	HNW24X	adhesion molecule
271	94.5	4.5	588	2	JH0506	surface glycoprote
272	94.5	4.5	588	2	A45254	hypothetical prote
273	94.5	4.5	875	2	T33434	ufo protein - mous
274	94.5	4.5	888	2	S23065	novel cellular pro
275	94.5	4.5	999	2	I38547	MHC class II I-A-a
276	94	4.5	118	2	I71934	Ig heavy chain V r
277	94	4.5	268	2	A56446	hemagglutinin - va
278	94	4.5	313	2	H36854	glial growth facto
279	94	4.5	422	2	S32357	probable PTR2 fami
280	94	4.5	583	2	G84829	ATP-dependent RNA
281	94	4.5	943	2	F69543	contactin precursor
282	94	4.5	1091	2	S01998	yxek protein - Bac
283	94	4.5	1325	2	A64905	probable membrane
284	94	4.5	1648	2	S61654	T-cell receptor de
285	93.5	4.5	142	2	S36307	ST2V protein - hum
286	93.5	4.5	259	2	JC7109	CD86 precursor - r
287	93.5	4.5	330	2	I46691	DM-GRASP precursor
288	93.5	4.5	587	2	JH0464	fibroblast growth
289	93.5	4.5	799	2	S18209	protein RanBP7 - A
290	93.5	4.5	1038	2	T30304	CDO protein - huma
291	93.5	4.5	1240	2	T03097	teratocarcinoma gl
292	93	4.4	330	2	A29915	T-cell surface gly
293	93	4.4	432	1	RWC2T4	pregnancy-specific
294	93	4.4	435	2	D33258	Ig mu chain C regi
295	93	4.4	568	2	A45804	hypothetical prote
296	93	4.4	625	2	T16777	neural adhesion pr
297	93	4.4	1018	2	JC4211	DNA-directed DNA p
298	93	4.4	1094	2	S22573	versican precursor
299	93	4.4	1643	2	T14274	T-cell receptor de
300	93	4.4	3381	2	T42389	CD86 spliced varia
301	92.5	4.4	144	2	S36322	pregnancy-specific
302	92.5	4.4	275	2	JC7604	brain-derived neur
303	92.5	4.4	424	2	A34595	brain-derived neur
304	92.5	4.4	474	1	C39667	secretory componen
305	92.5	4.4	476	1	B39667	brain-derived neur
306	92.5	4.4	764	1	QRHGS	T-cell receptor al
307	92.5	4.4	821	1	A39667	Ig light chain V r
308	92	4.4	116	2	E24891	tumor surface anti
309	92	4.4	132	2	A55410	alcam - human
310	92	4.4	323	2	A48997	Ig mu chain precur
311	92	4.4	583	2	I39428	cation-independent
312	92	4.4	627	2	S14683	insulin-like growt
313	92	4.4	1005	2	T18537	hypothetical prote
314	92	4.4	2482	2	I48922	antigen BCM1 precu
315	92	4.4	2483	1	A49617	interleukin-1 rece
316	92	4.4	13055	2	T16580	vascular cell adhe
317	91.5	4.4	240	2	JL0143	nephrin - human
318	91.5	4.4	576	2	A32604	probable multifunc
319	91.5	4.4	647	2	B41288	
320	91.5	4.4	1241	2	T37190	
321	91.5	4.4	1462	1	A69809	
322	91.5	4.4	2013	2	A11489	probable peptidogl
323	91	4.3	282	2	T17219	hypothetical prote
324	91	4.3	789	2	T28714	hypothetical prote
325	91	4.3	829	1	IJHUCP	cadherin 3 precurs
326	91	4.3	1355	2	T28715	hypothetical prote
327	90.5	4.3	309	2	S15674	cell surface glyco
328	90.5	4.3	341	2	B95403	probable ABC trans
329	90.5	4.3	361	2	PNO020	fibroblast growth
330	90.5	4.3	449	2	A45557	matrix, capsid, nu
331	90.5	4.3	452	1	MHHU	Ig mu chain C regi
332	90.5	4.3	453	2	S37768	Ig mu chain C regi
333	90.5	4.3	473	1	MHHUM	Ig mu chain C regi
334	90.5	4.3	487	2	S65133	butyrophilin - mou
335	90.5	4.3	531	2	S20900	titin - mouse (fra
336	90.5	4.3	631	1	A48346	cell fusion glycop
337	90.5	4.3	631	1	VGNZPD	cell fusion glycop
338	90.5	4.3	860	2	JC5702	ErbB kinase activa
339	90.5	4.3	868	2	JC5701	ErbB kinase activa
340	90	4.3	526	2	T27581	hypothetical prote
341	90	4.3	682	2	A35969	heparin-binding gr
342	90	4.3	821	1	TVHUF2	fibroblast growth
343	90	4.3	1018	2	A54744	contactin 1 precur
344	90	4.3	1343	2	E90893	hypothetical prote
345	90	4.3	1343	2	D85724	hypothetical prote
346	89.5	4.3	142	2	S04664	T-cell receptor de
347	89.5	4.3	157	2	S04915	T-cell receptor de
348	89.5	4.3	243	2	A37982	calcium vector pro
349	89.5	4.3	275	2	A28928	pregnancy-specific
350	89.5	4.3	335	2	H43354	pregnancy-specific
351	89.5	4.3	823	2	B35963	protein-tyrosine k
352	89.5	4.3	1465	2	S43528	165K protein, skel
353	89.5	4.3	2325	2	A61208	chondroitin sulfat
354	89	4.2	101	2	A29165	proteoglycan link
355	89	4.2	145	2	I46629	rearranged T-cell
356	89	4.2	279	2	S04693	T-cell receptor de
357	89	4.2	282	2	C28928	pregnancy-specific
358	89	4.2	413	1	IKBC5A	colicin V secretio
359	89	4.2	523	2	I50478	neurotin - goldfis
360	89	4.2	769	2	S16236	fibroblast growth
361	89	4.2	822	2	A45081	fibroblast growth
362	89	4.2	822	2	A41794	keratinocyte growt
363	89	4.2	822	2	S19947	fibroblast growth
364	89	4.2	822	2	B49151	protein-tyrosine k
365	89	4.2	941	1	TYWVMD	neuron cell surf
366	89	4.2	1020	1	S05944	leukocyte common a
367	89	4.2	1273	1	TDRTLT	insulin-like growt
368	89	4.2	2491	1	A28372	ketlin - fruit fly
369	88.5	4.2	524	2	S35341	probable envelope
370	88.5	4.2	975	2	T42576	peptidoglycan link
371	88.5	4.2	1711	2	AB1283	chondroitin sulfat
372	88.5	4.2	3562	2	A47171	hypothetical prote
373	88	4.2	131	2	T20334	myelin/oligodendro
374	88	4.2	247	2	A55717	T-cell surface gly
375	88	4.2	344	1	RMWTC2	hypothetical prote
376	88	4.2	691	2	T25519	hypothetical prote
377	88	4.2	769	1	QRRTGS	secretory componen
378	88	4.2	850	2	JC5700	ErbB kinase activa
379	88	4.2	1021	2	A57112	contactin precursor
380	88	4.2	1043	2	F97302	hypothetical prote
381	88	4.2	1451	2	S42167	190K protein - hum
382	88	4.2	2051	2	T30938	receptor tyrosine
383	87.5	4.2	205	2	A48929	activated B-cell p
384	87.5	4.2	246	2	A47712	myelin/oligodendro
385	87.5	4.2	474	2	S15590	Ig heavy chain - h
386	87.5	4.2	508	2	A33378	fasciclin III prec
387	87.5	4.2	742	2	J50326	alcohol dehydrogen
388	87.5	4.2	757	2	I45956	polymorphic immunog
389	87.5	4.2	768	2	A29066	DNA ligase (ATP) (
390	87.5	4.2	1197	2	T30581	neural cell adhesi
391	87.5	4.2	1417	2	H90670	probable invasion (
392	87.5	4.2	1417	2	D85521	probable adhesion e
393	87.5	4.2	1493	2	T10757	MAP kinase kinase
394	87.5	4.2	1897	1	TDHULK	leukocyte antigen-

395	87	4.1	139	2	S36302	T-cell receptor de
396	87	4.1	365	2	I72171	HLA-Aw33.1, HLA-Aw
397	87	4.1	707	2	UC7763	neuronal leucine-r
398	87	4.1	818	2	T19120	hypothetical prote
399	87	4.1	936	2	I40711	sapB protein - Cam
400	87	4.1	1042	2	A97209	spoIID-like domain
401	87	4.1	1957	2	T38077	hypothetical coile
402	86.5	4.1	115	2	C24891	T-cell receptor al
403	86.5	4.1	310	1	HNWZRA	hemagglutinin prec
404	86.5	4.1	363	2	JH0542	class I histocompa
405	86.5	4.1	465	2	A82211	MutT/nudix family
406	86.5	4.1	894	1	A41527	protein-tyrosine k
407	86.5	4.1	1348	2	S51656	vascular endotheli
408	86.5	4.1	1363	2	I58375	protein-tyrosine k
409	86.5	4.1	1637	2	T46438	hypothetical prote
410	86.5	4.1	1894	2	C54689	protein-tyrosine-p
411	86.5	4.1	3157	2	B70969	probable PPE prote
412	86	4.1	116	2	B24891	T-cell receptor al
413	86	4.1	150	2	I46624	rearranged T-cell
414	86	4.1	270	2	A34636	Fc-gamma receptor
415	86	4.1	357	2	S09265	Ig alpha chain C r
416	86	4.1	398	2	S17428	interleukin-1 rece
417	86	4.1	421	2	T46266	hypothetical prote
418	86	4.1	480	2	B56182	fibroblast growth
419	86	4.1	497	2	JC2456	pyruvate kinase (B
420	86	4.1	650	2	S22835	alpha-agglutinin -
421	86	4.1	964	2	T15746	hypothetical prote
422	86	4.1	975	1	TVMSKT	protein-tyrosine k
423	86	4.1	980	1	TVCTMD	macrophage colony-
424	86	4.1	1241	2	H84486	probable helicase
425	86	4.1	1327	2	T09402	immunoglobulin-lik
426	86	4.1	1345	2	H90975	hypothetical prote
427	86	4.1	2660	2	E85822	probable invasin Z
428	85.5	4.1	210	2	A56169	Ig kappa chain V r
429	85.5	4.1	216	2	JE0245	Ig lambda chain NI
430	85.5	4.1	218	2	S68241	Ig kappa chain V r
431	85.5	4.1	302	2	C36464	fibroblast growth
432	85.5	4.1	329	2	A44065	fibroblast growth
433	85.5	4.1	332	2	C36610	sulfate-binding pr
434	85.5	4.1	388	2	B48899	beta-lactamase (BC
435	85.5	4.1	397	2	C43354	pregnancy-specific
436	85.5	4.1	419	2	JC4123	pregnancy-specific
437	85.5	4.1	869	2	A86983	conserved hypothet
438	85.5	4.1	869	2	S72760	ppsl protein - Myc
439	85.5	4.1	1002	2	T19226	hypothetical prote
440	85.5	4.1	1028	2	C68364	protein C13B4.1 [i
441	85.5	4.1	1518	2	S37928	probable purine nu
442	85.5	4.1	1691	1	D54689	protein-tyrosine-p
443	85.5	4.1	2541	2	T29340	hypothetical prote
444	85	4.1	104	2	S07705	T-cell receptor al
445	85	4.1	137	2	S36303	T-cell receptor de
446	85	4.1	166	2	A33402	pregnancy-specific
447	85	4.1	247	2	S58394	myelin/oligodendro
448	85	4.1	265	2	A55811	carcinoembryonic a
449	85	4.1	273	2	B28928	pregnancy-specific
450	85	4.1	324	2	G43354	pregnancy-specific
451	85	4.1	326	2	F43354	pregnancy-specific
452	85	4.1	333	2	A43354	pregnancy-specific
453	85	4.1	428	2	I57486	pregnancy-specific
454	85	4.1	428	2	J50032	pregnancy-specific
455	85	4.1	480	2	A56182	fibroblast growth
456	85	4.1	496	2	PQ0666	envelope protein -
457	85	4.1	669	2	T51246	ARL1 protein limpo
458	85	4.1	776	2	S41628	genome polyprotein
459	85	4.1	781	2	S51592	Xyrb precursor - R
460	85	4.1	821	1	TVMSBK	fibroblast growth
461	85	4.1	904	2	I38757	homolog of Drosoph
462	85	4.1	913	1	A47543	R-cadherin precurs
463	85	4.1	926	2	I38756	homolog of Drosoph
464	85	4.1	1005	2	A42265	alpha-mannosidase
465	85	4.1	1216	2	S60613	protein-tyrosine-p
466	85	4.1	2409	1	A60979	versican precursor
467	85	4.1	4116	2	T13719	calo protein - fru
468	84.5	4.0	241	2	S32359	glial growth facto
469	84.5	4.0	264	2	F27579	T-cell receptor al
470	84.5	4.0	266	2	T29613	hypothetical prote
471	84.5	4.0	286	2	A28333	carcinoembryonic a
472	84.5	4.0	419	2	A33258	pregnancy-specific
473	84.5	4.0	419	2	A31135	pregnancy-specific
474	84.5	4.0	432	2	S30193	T-cell surface gly
475	84.5	4.0	436	2	B69371	bile acid-inducibl
476	84.5	4.0	457	2	A27449	T-cell surface gly
477	84.5	4.0	568	2	I58106	gene DMR-N9 protei
478	84.5	4.0	642	2	E72215	oligopeptide ABC t
479	84.5	4.0	795	2	T21487	hypothetical prote
480	84.5	4.0	874	2	E97302	hypothetical prote
481	84.5	4.0	1142	2	A11476	myosin-binding pro
482	84.5	4.0	1349	2	A11476	cell surface prote
483	84.5	4.0	1433	2	T30261	chitinase (BC 3.2.
484	84.5	4.0	2508	2	S61441	surface-associated
485	84	4.0	238	2	C90909	probable major tai
486	84	4.0	255	2	JC7593	SH2 domain-contain
487	84	4.0	315	1	HNWZVT	hemagglutinin prec
488	84	4.0	315	2	T37438	hemagglutinin - va
489	84	4.0	317	2	TL0118	Fc gamma (IgG) rec
490	84	4.0	321	2	D39371	Ig V-region-like B
491	84	4.0	336	2	S42632	Fit-1S protein pre
492	84	4.0	381	2	I51174	Ig heavy chain - R
493	84	4.0	402	2	T09062	probable advanced
494	84	4.0	406	2	E43354	pregnancy-specific
495	84	4.0	473	2	T35997	conserved hypothet
496	84	4.0	621	2	B57431	myosin-binding C-p
497	84	4.0	621	2	B57431	fibroblast growth
498	84	4.0	705	2	S51635	keratinocyte growt
499	84	4.0	707	2	A38442	hypothetical prote
500	84	4.0	939	2	AF2503	protein-tyrosine k
501	84	4.0	977	2	I45877	protein C18F3.2 [i
502	84	4.0	987	2	A88746	NoIG efflux transp
503	84	4.0	1065	2	H95321	hypothetical prote
504	84	4.0	1287	2	T30988	protein-tyrosine-p
505	84	4.0	1912	2	A56178	versican precursor
506	83.5	4.0	2397	1	A55535	T-cell receptor al
507	83.5	4.0	275	1	RWHUAC	B-cell-restricted
508	83.5	4.0	288	2	A45803	exported sulfate-b
509	83.5	4.0	329	2	AG0010	Ig alpha chain C r
510	83.5	4.0	339	2	S09264	class I histocompa
511	83.5	4.0	363	2	S07113	Ig V-region-like B
512	83.5	4.0	372	2	C39371	envelope protein B
513	83.5	4.0	496	2	S60685	LAG-3 protein prec
514	83.5	4.0	498	2	S11246	hypothetical prote
515	83.5	4.0	527	2	D75127	hypothetical prote
516	83.5	4.0	527	2	I56526	interleukin 1 rece
517	83.5	4.0	590	2	AE1525	probable peptidogl
518	83.5	4.0	629	2	S41050	fibroblast growth
519	83.5	4.0	748	2	S41051	fibroblast growth
520	83.5	4.0	911	2	I05360	synapse-associated
521	83.5	4.0	916	2	T05360	probable potassium
522	83.5	4.0	976	1	TVHUKT	protein-tyrosine k
523	83.5	4.0	1032	2	T34433	hypothetical prote
524	83.5	4.0	2163	2	T15276	hypothetical prote
525	83.5	4.0	2232	2	T34434	genome polyprotein
526	83.5	4.0	3898	1	GNWVHC	T-cell receptor de
527	83	4.0	115	2	B32071	Ig lambda chain -
528	83	4.0	115	2	S25747	hypothetical prote
529	83	4.0	416	2	G83656	conserved domain p
530	83	4.0	422	2	B95001	pregnancy-specific
531	83	4.0	445	2	A97873	conserved hypothet
532	83	4.0	977	2	S49004	tyrosine kinase Mp
533	83	4.0	1151	2	A57064	integrin alpha-1 c
534	83	4.0	1188	1	A45226	protein-tyrosine-p
535	83	4.0	1211	2	S68251	phospholipase C, 1
536	83	4.0	2302	2	T14328	protein-tyrosine-p
537	83	4.0	3029	2	S76109	hypothetical prote
538	82.5	3.9	185	2	S37479	T-cell receptor al
539	82.5	3.9	218	2	UC5810	monoclonal antibod
540	82.5	3.9	218	2	B47712	myelin/oligodendro

541 82.5 3.9 229 2 A46527 B-cell-specific me
542 82.5 3.9 230 2 A56210 neu differentiatio
543 82.5 3.9 304 2 F87701 histone deacetylase
544 82.5 3.9 316 2 C37028 MHC class I histoc
545 82.5 3.9 353 2 S51242 heparin-binding fi
546 82.5 3.9 355 2 I80169 class I histocompa
547 82.5 3.9 356 1 S55437 translation releas
548 82.5 3.9 395 2 D43354 pregnancy-specific
549 82.5 3.9 417 2 A28277 pregnancy-specific
550 82.5 3.9 453 2 B83380 hypothetical prote
551 82.5 3.9 509 2 JC5288 SHP substrate-1 pr
552 82.5 3.9 513 2 JC5289 SHP substrate-1 pr
553 82.5 3.9 640 2 B84478 probable replicati
554 82.5 3.9 651 2 A96781 unknown protein F9
555 82.5 3.9 666 2 D82511 1,4-alpha-glucan b
556 82.5 3.9 757 1 S48841 secretory componen
557 82.5 3.9 793 2 S59067 penton long fiber
558 82.5 3.9 942 2 S23251 protein-tyrosine k
559 82.5 3.9 1015 2 T32186 hypothetical prote
560 82 3.9 147 2 I46625 rearranged T-cell
561 82 3.9 150 2 S36312 T-cell receptor de
562 82 3.9 230 2 S26199 plastoquinol-plast
563 82 3.9 242 2 S06942 hypothetical prote
564 82 3.9 250 2 H81854 probable zinc-bind
565 82 3.9 261 2 C85681 hypothetical prote
566 82 3.9 335 2 A33514 pregnancy-specific
567 82 3.9 340 2 T28137 Ig V-region-like B
568 82 3.9 352 2 S09266 Ig alpha chain C r
569 82 3.9 374 2 F69233 carbamoyl-phosphat
570 82 3.9 426 2 C55181 pregnancy-specific
571 82 3.9 426 2 S09016 pregnancy-specific
572 82 3.9 436 2 B35334 pregnancy-specific
573 82 3.9 436 2 B55181 pregnancy-specific
574 82 3.9 684 2 F97148 aldehyde:ferredoxi
575 82 3.9 704 2 T31227 tran protein homol
576 82 3.9 707 2 A54846 fibroblast growth
577 82 3.9 822 2 B54846 fibroblast growth
578 82 3.9 1086 2 AF1662 cellobiose-phospho
579 82 3.9 1160 2 F88369 protein unc-52 (im
580 82 3.9 1198 2 T49726 hypothetical prote
581 82 3.9 1378 1 I48751 protein-tyrosine k
582 82 3.9 1385 2 D89824 hypothetical prote
583 82 3.9 1778 2 AF1116 internalin protein
584 82 3.9 1832 2 T31113 mucin-like glycopr
585 82 3.9 1898 2 S46216 leukocyte antigen-
586 82 3.9 4006 2 T09070 probable tenascin
587 81.5 3.9 85 2 S08109 carcinoembryonic a
588 81.5 3.9 140 2 C24747 T-cell receptor be
589 81.5 3.9 213 2 S68213 Ig heavy chain (Ma
590 81.5 3.9 235 2 I50610 T-cell surface gly
591 81.5 3.9 283 1 FCM5G1 Fc gamma (IgG) rec
592 81.5 3.9 314 1 HNVZVW hemagglutinin prec
593 81.5 3.9 314 1 JQ1793 hemagglutinin prec
594 81.5 3.9 339 2 T28138 Ig V-region-like B
595 81.5 3.9 426 2 A35964 pregnancy-specific
596 81.5 3.9 650 1 JC1450 fibroblast growth
597 81.5 3.9 687 2 A49636 soluble vascular e
598 81.5 3.9 699 2 A12686 proteinase II limp
599 81.5 3.9 699 2 E97468 dipeptidyl aminope
600 81.5 3.9 1015 2 T32984 hypothetical prote
601 81.5 3.9 3507 2 T34513 hypothetical prote
602 81 3.9 117 2 S49983 Tcell receptor alp
603 81 3.9 139 2 I46630 rearranged T-cell
604 81 3.9 145 2 I46631 rearranged T-cell
605 81 3.9 206 2 A40305 biliary glycoprote
606 81 3.9 315 1 HNVZVW hemagglutinin prec
607 81 3.9 432 1 RWMQ74 T-cell surface gly
608 81 3.9 438 2 E96545 hypothetical prote
609 81 3.9 450 2 S25162 gag protein - feil
610 81 3.9 509 2 JC6203 SP8 binding protei
611 81 3.9 645 2 T49702 related to DOS1 pr
612 81 3.9 673 2 S46520 luciferin-binding
613 81 3.9 767 2 F86383 hypothetical prote

614 615 81 3.9 823 2 S44873
616 617 81 3.9 846 2 T19179
618 619 81 3.9 978 1 A49814
620 621 81 3.9 990 2 T16554
622 623 81 3.9 1001 2 T00532
624 625 81 3.9 1102 2 F84572
626 627 81 3.9 1433 1 A36734
628 629 81 3.9 1433 1 A36734
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632 633 81 3.9 1433 1 A36734
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682 683 81 3.9 1433 1 A36734
684 685 81 3.9 1433 1 A36734
686 687 81 3.9 1433 1 A36734

2C21.2 protein - C
hypothetical prote
protein-tyrosine k
hypothetical prote
probable cadmium-t
probable cadmium-t
bacillopeptidase F
protein J⁺ - Yersin
phage lambda-relat
dominant autoantib
probable peptidogl
hypothetical prote
T cell receptor CK
VpreB protein prec
MHC class I histoc
pregnancy-specific
pregnancy-specific
interleukin-2 rece
transferrin-bindin
fibroblast growth
hypothetical prote
endo-beta-N-acetyl
protein-tyrosine k
large chain of NAD
conserved hypotet
probable type II s
rearranged T-cell
T-cell receptor al
hypothetical prote
Ig heavy chain V-I
mitosis-specific c
cell surface glyco
B-lymphocyte activ
MHC class I histoc
flagellar hook pro
Ig heavy chain pro
peptidylprolyl iso
hypothetical prote
probable secreted
surface-array prot
hypothetical prote
Ca2+-transporting
myosin-binding pro
hypothetical prote
fibronectin - Afri
hypothetical prote
T-cell receptor de
T-cell receptor al
T-cell receptor de
T-cell receptor al
hypothetical prote
rearranged T-cell
rearranged T-cell
Ig lambda chain -
fibroblast growth
B7 protein - red-c
MHC ChLA chain - c
Ig alpha chain C r
mitosis-specific c
Ig alpha chain C r
actin 2 - Arabidop
phosphate-binding
exodeoxyribonuclea
G-protein signalin
isocitrate dehydro
pregnancy-specific
muscarinic acetylch
peptide transport-
dihydroilipoamide S
hypothetical prote

687	79.5	3.8	974	2	S34189	starch phosphoryla
688	79.5	3.8	1209	2	T14357	homeodomain-intera
689	79.5	3.8	1251	2	T21389	hypothetical prote
690	79.5	3.8	1265	1	A37967	neural cell adhesi
691	79.5	3.8	1663	1	C3RT	complement C3 prec
692	79.5	3.8	2218	2	B84683	hypothetical prote
693	79.5	3.8	3600	2	D86161	Fl1003.12 protein -
694	79	3.8	118	2	S04519	Ig lambda chain pr
695	79	3.8	132	2	PQ0060	T-cell receptor be
696	79	3.8	210	2	UC4122	pregnancy-specific
697	79	3.8	226	2	S25745	Ig lambda chain -
698	79	3.8	241	2	D43273	heregulin precursor
699	79	3.8	345	2	A46052	vascular cell adhe
700	79	3.8	370	2	S29139	aggreccan - pig (fr
701	79	3.8	374	2	A46352	ORF1 protein - Chl
702	79	3.8	407	2	T08732	hypothetical prote
703	79	3.8	451	2	S71754	cellular hepatitis
704	79	3.8	502	2	T02746	cyclin A-like prot
705	79	3.8	567	2	S29498	lymphocyte antigen
706	79	3.8	716	1	WZBBE6	77.8k DNA helicase
707	79	3.8	741	2	E83265	probable two-compo
708	79	3.8	742	2	F84643	hypothetical prote
709	79	3.8	1250	2	E81339	probable restricti
710	79	3.8	1255	2	T06267	nematodes resistan
711	79	3.8	1298	2	A48999	protein-tyrosine k
712	79	3.8	1315	2	T28679	fibrinogen-binding
713	79	3.8	1388	2	T38720	chromodomain helic
714	79	3.8	3414	1	GNWVNE	genome polypeptide
715	78.5	3.7	136	2	JQ0473	T-cell receptor be
716	78.5	3.7	136	2	S36320	T-cell receptor de
717	78.5	3.7	215	2	A57843	sodium channel bet
718	78.5	3.7	230	2	S33161	Ig kappa chain - s
719	78.5	3.7	250	2	S11915	2',3'-cyclic-nucle
720	78.5	3.7	269	2	S57494	T-cell receptor al
721	78.5	3.7	270	2	S65739	basigin precursor
722	78.5	3.7	279	2	S53363	mucin 5AC (clone J
723	78.5	3.7	324	2	S36646	integrin-associate
724	78.5	3.7	335	2	A75363	inositol monophosp
725	78.5	3.7	355	2	S03537	class I histocompa
726	78.5	3.7	363	2	I37544	class I histocompa
727	78.5	3.7	366	2	S42823	MHC class I histoc
728	78.5	3.7	366	2	B37028	MHC class I histoc
729	78.5	3.7	407	2	C83589	MHC class I histoc
730	78.5	3.7	419	2	B54312	conserved hypotet
731	78.5	3.7	484	2	B64481	pregnancy-specific
732	78.5	3.7	568	2	A34891	hypothetical prote
733	78.5	3.7	592	2	S25705	Ig heavy chain pre
734	78.5	3.7	600	2	A82043	Ig mu chain - shee
735	78.5	3.7	612	2	B42755	inner membrane cop
736	78.5	3.7	612	2	S73873	E-selectin precurs
737	78.5	3.7	787	2	C38992	probable lipoprote
738	78.5	3.7	916	2	T22545	cadherin 4 precurs
739	78.5	3.7	1059	2	S60138	hypothetical prote
740	78.5	3.7	1243	2	S25345	sex factor aggrega
741	78.5	3.7	1609	2	T08437	probable membrane
742	78.5	3.7	2895	2	B98068	hyperplastic discs
743	78	3.7	95	2	A29080	hypothetical prote
744	78	3.7	121	2	C54312	T-cell receptor al
745	78	3.7	335	2	E71101	pregnancy-specific
746	78	3.7	342	2	AE3303	probable geranylge
747	78	3.7	367	2	JC4626	putrescine-binding
748	78	3.7	519	2	D14444	6-phosphofructo-2-
749	78	3.7	555	2	A95122	probable thioester
750	78	3.7	607	2	E64734	Tn5252, relaxase l
751	78	3.7	617	2	S60266	yach protein - Esc
752	78	3.7	684	2	T49136	novel antigen rece
753	78	3.7	841	2	S29605	killer cell inhibi
754	78	3.7	886	2	A42404	glycoprotein 350/2
755	78	3.7	941	2	T04294	protein kinase-lik
756	78	3.7	1185	2	S07245	collagen adhesin -
757	78	3.7	1203	2	T17414	hypothetical prote
758	78	3.7	1335	2		xanthine dehydroge
759	78	3.7	3848	2		tipc protein - sli
760	77.5	3.7	760	2	S36067	Ig lambda chain -
761	77.5	3.7	761	2	G24402	T-cell receptor al
762	77.5	3.7	762	2	S16439	Ig lambda chain -
763	77.5	3.7	763	2	A45893	T-cell receptor al
764	77.5	3.7	764	2	I83053	pregnancy-specific
765	77.5	3.7	765	2	A33937	Ig light chain (13
766	77.5	3.7	766	2	S25758	Ig lambda chain -
767	77.5	3.7	767	2	JC4121	pregnancy-specific
768	77.5	3.7	768	2	S29690	Ig heavy chain VDJ
769	77.5	3.7	769	2	A37412	T-cell receptor de
770	77.5	3.7	770	2	T18790	hypothetical prote
771	77.5	3.7	771	2	JN0067	pregnancy-specific
772	77.5	3.7	772	1	S42102	MHC class I histoc
773	77.5	3.7	773	2	S59931	glycerophosphodie
774	77.5	3.7	774	2	S59932	glycerophosphodie
775	77.5	3.7	775	2	S59933	glycerophosphodie
776	77.5	3.7	776	2	A43576	glycerophosphodie
777	77.5	3.7	777	2	S59934	leukostatin precur
778	77.5	3.7	778	2	H84182	hypothetical prote
779	77.5	3.7	779	2	B84540	acid phosphatase (
780	77.5	3.7	780	1	S60686	envelope protein B
781	77.5	3.7	781	2	S17597	Ig delta chain (WI
782	77.5	3.7	782	2	A46611	myosin-binding pro
783	77.5	3.7	783	2	S49219	involved in polyke
784	77.5	3.7	784	2	H69678	hypothetical prote
785	77.5	3.7	785	2	T50013	hypothetical prote
786	77.5	3.7	786	2	T16525	meprin A (EC 3.4.2
787	77.5	3.7	787	2	A48040	hypothetical prote
788	77.5	3.7	788	2	C71513	CryIaC toxin-bindi
789	77.5	3.7	789	2	B87992	protein W09G3.1a (
790	77.5	3.7	790	2	T48358	hypothetical prote
791	77.5	3.7	791	2	B69368	hypothetical prote
792	77.5	3.7	792	2	T41343	probable translati
793	77.5	3.7	793	2	T23308	hypothetical prote
794	77.5	3.7	794	2	T26318	hypothetical prote
795	77.5	3.7	795	2	S12050	protein-tyrosine-p
796	77.5	3.7	796	1	I50726	cation-independent
797	77.5	3.7	797	2	D95201	hypothetical prote
798	77.5	3.7	798	2	JH0340	T-cell receptor al
799	77.5	3.7	799	2	S26512	T-cell receptor al
800	77	3.7	800	2	S36323	T-cell receptor de
801	77	3.7	801	2	T15747	hypothetical prote
802	77	3.7	802	2	E83687	hypothetical prote
803	77	3.7	803	2	T31517	hypothetical prote
804	77	3.7	804	2	F71624	Ig mu chain C regi
805	77	3.7	805	2	T45033	hypothetical prote
806	77	3.7	806	2	I52590	m33-B isoform - mo
807	77	3.7	807	2	T218143	tapasin 1 homolog,
808	77	3.7	808	2	T17289	dipeptidyl-peptida
809	77	3.7	809	2	A41158	hypothetical prote
810	77	3.7	810	2	T38444	envelope glycoprot
811	77	3.7	811	2	A43383	beta-D-glucan exoh
812	77	3.7	812	2	T51281	hypothetical prote
813	77	3.7	813	2	AB1129	methy1-accepting c
814	77	3.7	814	2	A42707	killer cell inhibi
815	77	3.7	815	2	S38001	hypothetical prote
816	77	3.7	816	1	S46122	Internalin A limpo
817	77	3.7	817	2	S46122	type II transposas
818	77	3.7	818	2	T07756	probable serine/th
819	77	3.7	819	2	T38393	SNF2 protein homol
820	77	3.7	820	2	A57036	phytochrome B - so
821	77	3.7	821	2	I38316	clathrin heavy cha
822	77	3.7	822	2	S03513	talain - slime mold
823	77	3.7	823	2	S36306	T-cell receptor de
824	77	3.7	824	2	I46626	T-cell receptor de
825	77	3.7	825	2	H86874	rearranged T-cell
826	77	3.7	826	2		50S ribosomal prot
827	77	3.7	827	2		
828	76.5	3.6	828	2		
829	76.5	3.6	829	2		
830	76.5	3.6	830	2		
831	76.5	3.6	831	2		
832	76.5	3.6	832	2		

833	76.5	3.6	239	2	G97165	flagellar hook ass	906	76	3.6	4660	2	T42737	gp330 protein prec
834	76.5	3.6	240	2	S01299	OX-45 membrane gly	907	75.5	3.6	116	2	S22558	Ig heavy chain V r
835	76.5	3.6	240	2	A39016	T-cell surface gly	908	75.5	3.6	146	2	H32536	T-cell receptor al
836	76.5	3.6	255	2	UQ1240	hypothetical 29.3k	909	75.5	3.6	275	2	PS0402	basigin type III -
837	76.5	3.6	296	2	B39581	GRESAG protein 9u	910	75.5	3.6	283	2	F87183	probable exported
838	76.5	3.6	299	2	I46690	CD80 precursor - r	911	75.5	3.6	297	2	AG2955	hypothetical prote
839	76.5	3.6	318	2	H75157	daunorubicin resis	912	75.5	3.6	297	2	F98327	hypothetical prote
840	76.5	3.6	330	2	A40071	Fc gamma (IgG) rec	913	75.5	3.6	312	2	H64560	probable tetraacyl
841	76.5	3.6	336	2	I48471	Fc gamma (IgG) rec	914	75.5	3.6	330	2	I49660	Ig alpha chain C r
842	76.5	3.6	404	2	A46480	Fc gamma (IgG) rec	915	75.5	3.6	342	2	A45966	MHC class I histoc
843	76.5	3.6	451	2	T30603	perlecan homolog 2	916	75.5	3.6	366	2	I37527	brevican precursor
844	76.5	3.6	477	2	H75026	oligopeptide abc t	917	75.5	3.6	371	2	A53908	Ig V-region-like B
845	76.5	3.6	501	2	A42030	alpha-globin trans	918	75.5	3.6	398	2	A39371	zinc finger protei
846	76.5	3.6	503	2	JC5287	SHP substrate-1 pr	919	75.5	3.6	459	2	T43538	transcription fact
847	76.5	3.6	530	2	T18596	hypothetical prote	920	75.5	3.6	502	2	C56205	dipeptide ABC tran
848	76.5	3.6	599	2	T15552	hypothetical prote	921	75.5	3.6	549	2	G69618	hypothetical prote
849	76.5	3.6	632	2	H83106	chemotactic transd	922	75.5	3.6	605	2	S48940	probable membrane
850	76.5	3.6	742	2	S38093	probable purine nu	923	75.5	3.6	636	2	S63131	complement subcomp
851	76.5	3.6	771	2	A83348	probable aldehyde	924	75.5	3.6	705	1	C1HURB	hypothetical prote
852	76.5	3.6	838	2	I45557	eyeless, long form	925	75.5	3.6	710	2	B71417	alcohol dehydrogen
853	76.5	3.6	868	2	D86349	hypothetical prote	926	75.5	3.6	742	2	A49340	transforming prote
854	76.5	3.6	874	2	C84513	Mutator-like trans	927	75.5	3.6	761	1	TVHUMB	AAA family ATPase
855	76.5	3.6	886	2	T10890	cysteine proteinas	928	75.5	3.6	769	2	E90158	cadherin-6B - chic
856	76.5	3.6	980	2	T49570	hypothetical prote	929	75.5	3.6	790	2	I50178	F-cadherin - Afri
857	76.5	3.6	1110	2	T19673	hypothetical prote	930	75.5	3.6	790	2	I51638	hypothetical prote
858	76.5	3.6	1131	2	T09701	phytochrome - Scot	931	75.5	3.6	796	2	T20393	hypothetical prote
859	76.5	3.6	1138	2	S24614	myosin-binding pro	932	75.5	3.6	830	2	T10545	probable achilla tr
860	76.5	3.6	1311	2	T33757	RNA polymerase bet	933	75.5	3.6	866	2	B85075	neurotrophic recep
861	76.5	3.6	1350	2	AF2005	alkaline phosphata	934	75.5	3.6	937	1	URHUAP	peptidylglycine mo
862	76.5	3.6	1365	2	T30198	probable sideropho	935	75.5	3.6	974	1	AF0739	exodeoxyribonuclea
863	76.5	3.6	2201	2	AH0095	T-cell receptor de	936	75.5	3.6	1042	2	T49433	zinc finger RNA bl
864	76.5	3.6	120	2	C26945	T-cell receptor al	937	75.5	3.6	1052	2	S14342	replicase 126K - o
865	76	3.6	133	2	F24402	T-cell receptor de	938	75.5	3.6	1112	2	T49432	hypothetical prote
866	76	3.6	141	2	S36318	Ig lambda chain -	939	75.5	3.6	1294	2	T04278	hypothetical prote
867	76	3.6	145	2	S25743	T-cell receptor de	940	75.5	3.6	1662	2	T01893	cell surface antigen
868	76	3.6	149	2	S36317	Fc gamma (IgG) rec	941	75.5	3.6	1902	2	C97702	genome polypeptide
869	76	3.6	323	2	S06946	CAMP response elem	942	75.5	3.6	2333	1	GNNY2F	unknown protein Fl
870	76	3.6	341	2	S26686	MHC class I histoc	943	75	3.6	2599	2	A96616	T-cell receptor al
871	76	3.6	360	2	A27638	HLA-B*5602 - human	944	75	3.6	132	1	RMMSAV	T-cell receptor be
872	76	3.6	362	2	I72755	HLA-B*5601 - human	945	75	3.6	141	2	S38389	Ig kappa chain pre
873	76	3.6	362	2	I72754	MHC class I histoc	946	75	3.6	233	2	S25742	major tail protein
874	76	3.6	365	2	I38439	lymphocyte antigen	947	75	3.6	234	2	S01320	probable R1eske pr
875	76	3.6	366	2	I81231	Ig mu heavy chain	948	75	3.6	238	2	D90876	probable tail comp
876	76	3.6	391	1	MHHUBT	probable acyl-CoA	949	75	3.6	252	2	H72554	nonspecific proteinas
877	76	3.6	400	2	AD3364	branched-chain ami	950	75	3.6	301	2	AC3476	alcohol dehydrogen
878	76	3.6	401	2	AG3552	alpha-methylacyl-C	951	75	3.6	335	2	B33251	hypothetical prote
879	76	3.6	415	2	AB3637	hypothetical prote	952	75	3.6	346	2	C81088	MHC class I histoc
880	76	3.6	441	2	H96817	hypothetical prote	953	75	3.6	360	2	AB1931	MHC class I histoc
881	76	3.6	443	2	A96818	hypothetical prote	954	75	3.6	362	2	I37120	MHC class I histoc
882	76	3.6	446	2	F84451	probable uridylyl	955	75	3.6	362	2	B30345	MHC class I histoc
883	76	3.6	457	1	RMMS74	T-cell surface gly	956	75	3.6	362	2	I37522	MHC class I histoc
884	76	3.6	478	2	AF1758	chitinase and chit	957	75	3.6	362	2	I61904	MHC class I histoc
885	76	3.6	496	2	PC4408	protein E - Tick-b	958	75	3.6	362	2	I54457	MHC class I histoc
886	76	3.6	507	2	S52348	hypothetical prote	959	75	3.6	362	2	A30345	MHC class I histoc
887	76	3.6	511	2	A97212	protein containing	960	75	3.6	367	2	S15716	pectate lyase (EC
888	76	3.6	519	2	S71451	halolysin R4 (EC 3	961	75	3.6	387	2	H65132	hypothetical 44.3
889	76	3.6	555	2	T01142	hypothetical prote	962	75	3.6	396	2	C95088	S-adenosylmethionl
890	76	3.6	562	2	A65166	hypothetical 63.2K	963	75	3.6	396	2	G97955	methionine adenosyl
891	76	3.6	562	2	B91194	probable enzyme [i	964	75	3.6	404	1	JQ1531	nucleoprotein - he
892	76	3.6	562	2	C86041	hypothetical prote	965	75	3.6	450	1	FOLJFP	gag polypeptide -
893	76	3.6	609	2	T16135	hypothetical prote	966	75	3.6	450	1	S23819	gag protein - feli
894	76	3.6	649	2	T32755	hypothetical prote	967	75	3.6	471	2	B38637	Ras inhibitor (clo
895	76	3.6	723	2	S40127	probable coat prot	968	75	3.6	483	2	A69745	hypothetical prote
896	76	3.6	800	2	S37387	internalin A precu	969	75	3.6	496	2	PQ0508	envelope glycoprot
897	76	3.6	871	2	T45692	receptor-like prote	970	75	3.6	496	2	E90181	hypothetical prote
898	76	3.6	959	1	P2XR13	outer capsid prote	971	75	3.6	507	2	AE0473	colicin (partial)
899	76	3.6	1245	2	T49815	related to multifu	972	75	3.6	519	2	T39641	conserved hypothet
900	76	3.6	1497	2	I49607	procollagen type V	973	75	3.6	547	2	A70038	L-lactate permease
901	76	3.6	1537	2	JC4172	DNA (cytosine-5-)-	974	75	3.6	563	2	A34341	poly(3-hydroxybuty
902	76	3.6	2332	1	GNNY4F	genome polypeptide	975	75	3.6	589	2	JC7992	negatively regulat
903	76	3.6	2499	1	A30788	mannose 6-phosphat	976	75	3.6	613	2	F85074	hypothetical prote
904	76	3.6	2550	2	B53435	vesicular transpor	977	75	3.6	630	2		
905	76	3.6	3716	2	E70969	probable ppe prote	978	75	3.6		2		

979	75	3.6	632	2	S73431	MG288 homolog D09_	1052	74.5	3.6	2143	2	G96595	hypothetical prote
980	75	3.6	669	2	S46519	luciferin-binding	1053	74.5	3.6	3890	2	C89921	hypothetical prote
981	75	3.6	669	2	S46518	luciferin-binding	1054	74.5	3.6	4436	2	E71086	hypothetical prote
982	75	3.6	686	2	JC7569	Delta-4 protein -	1055	74.5	3.6	4861	2	S71752	giant protein p619
983	75	3.6	808	2	T23129	hypothetical prote	1056	74	3.5	115	2	A30583	T-cell receptor de
984	75	3.6	997	2	A40812	Ca2+-transporting	1057	74	3.5	130	2	S08079	Ig kappa chain pre
985	75	3.6	999	2	A34307	Ca2+-transporting	1058	74	3.5	143	2	S36321	T-cell receptor de
986	75	3.6	1042	2	B40812	Ca2+-transporting	1059	74	3.5	145	2	S36299	T-cell receptor de
987	75	3.6	1118	1	A49724	protein-tyrosine-p	1060	74	3.5	217	2	J80246	Ig lambda chain NI
988	75	3.6	1144	2	T21223	hypothetical prote	1061	74	3.5	256	1	QQOMC2	B256 protein - cas
989	75	3.6	1234	2	S72640	endo-1,4-beta-xyla	1062	74	3.5	264	2	T26976	hypothetical prote
990	75	3.6	1241	2	S26373	genome polypeptide	1063	74	3.5	270	1	S77085	molybdate-binding
991	75	3.6	1277	2	T14152	synaptic scaffoldi	1064	74	3.5	285	2	S36903	Fc gamma (IgG) rec
992	75	3.6	1280	2	T29021	hypothetical prote	1065	74	3.5	318	2	C71197	probable ATP-bindi
993	75	3.6	1331	1	XORTDH	xanthine dehydroge	1066	74	3.5	327	2	F87544	UDP-glucose 4-epim
994	75	3.6	1448	2	AI2007	Subtilase family p	1067	74	3.5	330	2	AE3119	ABC transporter, s
995	75	3.6	1622	2	AE1717	probable cell surf	1068	74	3.5	339	2	JC7509	glycoprotein VI-1
996	75	3.6	2109	1	I50421	aggreccan precursor	1069	74	3.5	341	2	S20827	cAMP response elem
997	75	3.6	2124	2	A28452	proteoglycan core	1070	74	3.5	351	2	S78042	Ig mu chain C regi
998	75	3.6	2132	1	A55182	aggreccan precursor	1071	74	3.5	353	2	C86932	conserved hypothet
999	75	3.6	2415	1	A39086	aggreccan precursor	1072	74	3.5	354	2	S24436	class I histocompa
1000	75	3.6	3216	2	C90538	hypothetical prote	1073	74	3.5	362	2	I56130	HLA-B*5401 - human
1001	75	3.6	3263	2	E82410	hypothetical prote	1074	74	3.5	362	2	I59633	MHC HLA-B transmem
1002	75	3.6	3624	2	AD0835	large repetitive p	1075	74	3.5	362	2	I72753	HLA-B*5502 - human
1003	75	3.6	3712	1	YGCVC	alpha-aminodipyl-	1076	74	3.5	362	2	S24434	class I histocompa
1004	75	3.6	3947	2	T52486	ferrichrome sidero	1077	74	3.5	362	2	I72752	HLA-B*5501 - human
1005	74.5	3.6	115	2	A24891	T-cell receptor al	1078	74	3.5	362	2	I56133	MHC class I protei
1006	74.5	3.6	131	2	PQ0059	T-cell receptor be	1079	74	3.5	365	2	B95260	recf protein limpo
1007	74.5	3.6	133	2	S57885	T-cell receptor al	1080	74	3.5	365	2	E98125	recombination prot
1008	74.5	3.6	135	1	RWHUAV	T-cell receptor al	1081	74	3.5	379	2	T45768	periplasmic-iron-b
1009	74.5	3.6	142	1	E64794	ybdq protein - Esc	1082	74	3.5	387	2	B98168	isocitrate dehydro
1010	74.5	3.6	142	2	F90709	hypothetical prote	1083	74	3.5	425	2	E71982	probable membrane
1011	74.5	3.6	142	2	B85560	hypothetical prote	1084	74	3.5	430	2	S50981	Ig mu chain C regi
1012	74.5	3.6	208	2	B49444	Ig lambda chain (N	1085	74	3.5	450	1	MHDG	adhesin aidA-I lim
1013	74.5	3.6	212	2	C33258	pregnancy-specific	1086	74	3.5	487	2	AD3643	p-cadherin - bovin
1014	74.5	3.6	223	2	E64205	deoxyribose-phosph	1087	74	3.5	491	1	IJBOCP	4-coumarate-CoA li
1015	74.5	3.6	235	2	AD1735	hypothetical prote	1088	74	3.5	517	2	B87644	hypothetical prote
1016	74.5	3.6	294	2	T05381	hypothetical prote	1089	74	3.5	565	2	T47330	probable membrane
1017	74.5	3.6	345	2	C72760	probable heme expo	1090	74	3.5	617	2	A90644	probable membrane
1018	74.5	3.6	348	2	I50107	MHC class I histoc	1091	74	3.5	617	2	A85495	zinc finger protei
1019	74.5	3.6	361	2	B30461	MHC class I histoc	1092	74	3.5	626	2	I38618	glucan 1,3-beta-gl
1020	74.5	3.6	366	1	HLHW3	MHC class I histoc	1093	74	3.5	628	2	T51283	killer cell inhibi
1021	74.5	3.6	377	2	A49885	MHC class I histoc	1094	74	3.5	635	2	JC5896	hypothetical prote
1022	74.5	3.6	445	2	S43492	surface antigen -	1095	74	3.5	642	2	S58154	PES4 protein homol
1023	74.5	3.6	459	2	T37704	zinc-finger protei	1096	74	3.5	659	2	S46788	protein dim-1 limp
1024	74.5	3.6	476	2	A10189	exodeoxyribonuclea	1097	74	3.5	666	2	H89581	hypothetical prote
1025	74.5	3.6	503	2	AB1933	hypothetical prote	1098	74	3.5	708	2	T19474	transferrin-bindin
1026	74.5	3.6	536	2	T27668	hypothetical prote	1099	74	3.5	711	2	A90820	fibroblast growth
1027	74.5	3.6	560	2	D30930	flagellar basal bo	1100	74	3.5	813	1	A49123	disintegrin-like m
1028	74.5	3.6	596	2	S32802	apolipoprotein B -	1101	74	3.5	814	2	G02390	enhancing factor (
1029	74.5	3.6	604	2	AE2437	prolyl-tRNA synthe	1102	74	3.5	856	2	AD0042	C protein alpha an
1030	74.5	3.6	610	2	S52850	intermediate filam	1103	74	3.5	899	2	AG0859	DNA-directed DNA p
1031	74.5	3.6	652	2	G36560	hypothetical prote	1104	74	3.5	1020	2	A46405	fibronectin-bindin
1032	74.5	3.6	657	2	G83906	unknown protein li	1105	74	3.5	1084	1	S19661	pyruvate carboxyla
1033	74.5	3.6	706	2	D86441	DNA-directed RNA p	1106	74	3.5	1117	2	S33851	hypothetical prote
1034	74.5	3.6	717	2	B32838	ETS domain protein	1107	74	3.5	1144	2	D97227	xanthine dehydroge
1035	74.5	3.6	732	2	A43315	interleukin-4 rece	1108	74	3.5	1162	2	XOMSDH	protein-tyrosine-p
1036	74.5	3.6	782	2	T32155	CS3 pilin synthesi	1109	74	3.5	1335	1	S17670	multifunctional am
1037	74.5	3.6	810	1	A33380	neurotrophic recep	1110	74	3.5	1452	1	S18644	rifamycin polyketi
1038	74.5	3.6	937	2	S78561	nonB-dependent rec	1111	74	3.5	1714	1	S18644	genome polypeptid
1039	74.5	3.6	943	2	B45082	c-kit-related kina	1112	74	3.5	1763	2	T17465	Ig kappa chain V r
1040	74.5	3.6	946	2	B87316	mitotic control pr	1113	74	3.5	3412	1	GNWVTB	Ig kappa chain V r
1041	74.5	3.6	954	2	I51703	probable outer mem	1114	73.5	3.5	106	2	PL0267	Ig kappa chain V r
1042	74.5	3.6	1000	2	JE0110	hypothetical prote	1115	73.5	3.5	108	1	KVRBB5	Ig kappa chain V-
1043	74.5	3.6	1013	2	G71460	hypothetical prote	1116	73.5	3.5	111	1	L6HUST	T-cell receptor al
1044	74.5	3.6	1025	2	T21319	cellobiose-phospho	1117	73.5	3.5	111	2	JH0339	Ig kappa chain pre
1045	74.5	3.6	1086	2	AH1290	phytochrome B - po	1118	73.5	3.5	229	2	A20969	hypothetical prote
1046	74.5	3.6	1129	2	S28431	hypothetical prote	1119	73.5	3.5	245	2	T18609	Ig gamma chain - m
1047	74.5	3.6	1302	2	AC2574	probable membrane	1120	73.5	3.5	246	2	S38950	hypothetical prote
1048	74.5	3.6	1333	2	S63403	hypothetical prote	1121	73.5	3.5	253	2	T15475	basigin type II -
1049	74.5	3.6	1356	2	T16718	glutamate synthase	1122	73.5	3.5	257	2	PS0401	GP42/Basigin prote
1050	74.5	3.6	1446	2	T13018		1123	73.5	3.5	271	2	S43512	
1051	74.5	3.6	1615	2	C75551		1124	73.5	3.5	273	2	JX0107	

1125	73.5	3.5	284	2	A97203	2-oxoacid ferredox	1198	73	3.5	354	2	B82850	fimbrial adhesin p
1126	73.5	3.5	291	2	T30488	hypothetical prote	1199	73	3.5	362	1	HLHUB8	MHC class I histoc
1127	73.5	3.5	304	2	B88746	protein C18F3.3 (I	1200	73	3.5	362	2	A45834	MHC class I histoc
1128	73.5	3.5	310	2	HL0119	Fc gamma (IgG) rec	1201	73	3.5	362	2	T61907	MHC class I histoc
1129	73.5	3.5	316	2	H71231	molybdopterin bios	1202	73	3.5	362	2	A45850	MHC class I histoc
1130	73.5	3.5	325	2	I54449	MHC class I HLA-Cx	1203	73	3.5	362	2	I81233	lymphocyte antigen
1131	73.5	3.5	348	2	S09273	Ig alpha chain C r	1204	73	3.5	362	2	I84490	lymphocyte antigen
1132	73.5	3.5	351	2	B34595	pregnancy-specific	1205	73	3.5	362	2	A45880	MHC class I histoc
1133	73.5	3.5	351	2	A97064	D-mannosate hydrol	1206	73	3.5	362	2	I54442	MHC class I histoc
1134	73.5	3.5	357	2	D82337	UDP-N-acetylenolpy	1207	73	3.5	365	2	I37482	MHC class I histoc
1135	73.5	3.5	362	2	S68090	actin 8 - Arabidop	1208	73	3.5	378	2	S41870	surface antigen -
1136	73.5	3.5	364	1	OOHUR	opsin, red-sensiti	1209	73	3.5	402	2	CG9110	glutamate N-acetyl
1137	73.5	3.5	366	2	I68712	MHC class I histoc	1210	73	3.5	412	2	A41070	prolactin receptor
1138	73.5	3.5	366	2	F72062	hypothetical prote	1211	73	3.5	426	2	C72166	A22R protein - var
1139	73.5	3.5	366	2	A86561	CT449 hypothetical	1212	73	3.5	478	2	G75052	pyruvate kinase (B
1140	73.5	3.5	400	2	T34363	hypothetical prote	1213	73	3.5	478	2	T24805	hypothetical prote
1141	73.5	3.5	408	2	F81252	NADH2 dehydrogenas	1214	73	3.5	481	2	JC5378	protein disulfide-
1142	73.5	3.5	427	2	F64064	tolB protein - Hae	1215	73	3.5	489	2	T09151	glutathione-disulf
1143	73.5	3.5	446	2	S40295	Ig gamma-2a chain	1216	73	3.5	499	2	B86782	D-alanine activati
1144	73.5	3.5	482	2	T22754	hypothetical prote	1217	73	3.5	507	2	A48661	cystathionine beta
1145	73.5	3.5	487	1	A49760	fumarate hydratase	1218	73	3.5	508	2	B91250	hypothetical prote
1146	73.5	3.5	551	2	G84301	hypothetical prote	1219	73	3.5	521	2	B84746	hypothetical prote
1147	73.5	3.5	554	2	C70512	hypothetical prote	1220	73	3.5	580	2	AE1088	ABC transporter, A
1148	73.5	3.5	568	2	A89958	acetyl-CoA synthet	1221	73	3.5	610	2	A36116	prolactin receptor
1149	73.5	3.5	583	2	T02382	hypothetical prote	1222	73	3.5	615	2	T20839	hypothetical prote
1150	73.5	3.5	634	2	T51282	beta-D-glucan exoh	1223	73	3.5	681	2	A45055	glutamine-fructose
1151	73.5	3.5	659	2	A85854	hypothetical prote	1224	73	3.5	685	2	JC7570	MEK kinase - mouse
1152	73.5	3.5	659	2	G91009	colicin I receptor	1225	73	3.5	687	2	A46212	TPR-repeat-contain
1153	73.5	3.5	663	1	QRECIIC	colicin I receptor	1226	73	3.5	694	2	F97279	hypothetical prote
1154	73.5	3.5	694	2	F71514	probable translati	1227	73	3.5	771	2	T13618	hypothetical prote
1155	73.5	3.5	721	2	T05815	hypothetical prote	1228	73	3.5	796	2	D97065	transketolase (Imp
1156	73.5	3.5	737	2	T46243	hypothetical prote	1229	73	3.5	885	2	S42841	T16G12.1 protein -
1157	73.5	3.5	743	2	D64062	GTP diphosphokinas	1230	73	3.5	913	1	IJCHCR	R-cadherin precurs
1158	73.5	3.5	780	2	A34102	von Willebrand fac	1231	73	3.5	954	2	A10438	probable exported
1159	73.5	3.5	781	2	S57528	aconitlate hydratase	1232	73	3.5	998	2	H75005	ATP-dependent prot
1160	73.5	3.5	785	2	S54016	SOK2 protein - yea	1233	73	3.5	1071	2	B84062	hypothetical prote
1161	73.5	3.5	794	2	T36972	probable membrane	1234	73	3.5	1115	2	T29012	hypothetical prote
1162	73.5	3.5	886	2	E75625	hypothetical prote	1235	73	3.5	1122	2	T47424	hypothetical prote
1163	73.5	3.5	891	2	T19915	hypothetical prote	1236	73	3.5	1137	2	E86708	pyruvate carboxyla
1164	73.5	3.5	899	1	GNNVMVM	pol polypolypein -	1237	73	3.5	1144	2	A81983	probable DNA-direc
1165	73.5	3.5	923	2	S09583	peptidylglycine mo	1238	73	3.5	1177	2	T16594	hypothetical prote
1166	73.5	3.5	934	1	H71274	probable ankryrin -	1239	73	3.5	1199	2	T23005	hypothetical prote
1167	73.5	3.5	1102	2	H84545	probable ubiquitin	1240	73	3.5	1286	2	A88396	protein M01E10.2 f
1168	73.5	3.5	1127	1	E71156	endoropeptidase Ia h	1241	73	3.5	1289	2	C70044	probable phosphoes
1169	73.5	3.5	1133	1	GNVUSR	M polypolypein prec	1242	73	3.5	1293	2	B85557	enterobactin synth
1170	73.5	3.5	1133	2	S12597	M polypolypein prec	1243	73	3.5	1293	2	A90707	enterobactin synth
1171	73.5	3.5	1166	2	T28680	fibrinogen-binding	1244	73	3.5	1345	2	S55669	legument protein 7
1172	73.5	3.5	1193	2	T21133	hypothetical prote	1245	73	3.5	1390	1	TYHUME	hepatocyte growth
1173	73.5	3.5	1259	2	H65233	ytfn protein - Esc	1246	73	3.5	1407	1	T00558	probable ABC trans
1174	73.5	3.5	1293	1	YGECEF	enterobactin synth	1247	73	3.5	1437	2	T31093	probable protein-t
1175	73.5	3.5	1829	2	T24583	hypothetical prote	1248	73	3.5	1452	1	S71769	protein-tyrosine-p
1176	73.5	3.5	2761	2	T21064	hypothetical prote	1249	73	3.5	1484	2	T42632	breast cancer tumo
1177	73.5	3.5	2899	2	T21546	hypothetical prote	1250	73	3.5	1487	2	S62048	probable membrane
1178	73.5	3.5	2915	2	G87867	protein F36A2.13 f	1251	73	3.5	1615	2	B49502	ascites glialoglyco
1179	73.5	3.5	3097	2	T28635	glutamate synthase	1252	73	3.5	1630	2	A53577	mycocerosate synth
1180	73	3.5	107	2	B45722	anti-glycoprotein	1253	73	3.5	1767	2	A49502	genome polypolypein
1181	73	3.5	113	2	I46637	rearranged T-cell	1254	73	3.5	2118	2	S72705	enoyl-lacyl-carrie
1182	73	3.5	113	2	B49041	T-cell receptor al	1255	73	3.5	2142	1	ZLVNPFV	von Willebrand fac
1183	73	3.5	120	2	B25429	T-cell receptor be	1256	73	3.5	2505	1	XYRTFA	cyclosporin synthe
1184	73	3.5	126	2	B46538	Ig heavy chain, me	1257	73	3.5	2813	1	VWHTU	Ig lambda chain -
1185	73	3.5	131	1	L6HUEB	Ig lambda chain pr	1258	73	3.5	15281	2	S41309	T-cell receptor al
1186	73	3.5	135	2	S00388	T-cell receptor ga	1259	72.5	3.5	104	2	S36064	T-cell receptor al
1187	73	3.5	162	2	E71131	peptidylprolyl iso	1260	72.5	3.5	110	2	S23687	T-cell receptor al
1188	73	3.5	173	2	T27373	neu differentiatio	1261	72.5	3.5	110	2	S22897	Ig lambda chain V-
1189	73	3.5	175	2	I38408	sodium channel bet	1262	72.5	3.5	111	1	L6HULT	Ig lambda chain V-
1190	73	3.5	186	2	I61783	CD7 antigen - mous	1263	72.5	3.5	112	1	L1HUNA	T-cell receptor be
1191	73	3.5	210	2	I49294	Ig lambda chain V	1264	72.5	3.5	114	2	I38315	T-cell receptor be
1192	73	3.5	213	2	S21066	Ig heavy chain C r	1265	72.5	3.5	114	2	S03511	T-cell receptor be
1193	73	3.5	244	2	S12328	probable fimbrial	1266	72.5	3.5	115	2	S03510	T-cell receptor be
1194	73	3.5	247	2	AF0869	hypothetical prote	1267	72.5	3.5	115	2	A25777	T-cell receptor be
1195	73	3.5	251	2	T15495	PHP superfamily hy	1268	72.5	3.5	133	2	RWHUVY	T-cell receptor be
1196	73	3.5	253	2	G97267	T-cell receptor al	1269	72.5	3.5	135	1	S57877	T-cell receptor CK
1197	73	3.5	267	1	RMMSCH		1270	72.5	3.5	135	2		

1271	72.5	3.5	136	2	I46635	rearranged T-cell	1344	72	3.4	362	2	S24435	class I histocompa
1272	72.5	3.5	140	2	PH0132	Ig lambda chain pr	1345	72	3.4	362	2	S16789	class I histocompa
1273	72.5	3.5	224	2	B81783	hypothetical prote	1346	72	3.4	365	2	I72170	MHC class I histoc
1274	72.5	3.5	233	2	JH0372	42k surface glycop	1347	72	3.4	365	2	I38610	MHC class I histoc
1275	72.5	3.5	249	2	S69340	Ig heavy chain VHI	1348	72	3.4	369	2	S12406	glucan endo-1,3-be
1276	72.5	3.5	250	2	D83835	hypothetical prote	1349	72	3.4	386	2	A41950	retrovirus-related
1277	72.5	3.5	307	1	RWMSBC	T-cell receptor be	1350	72	3.4	392	2	D83513	probable esterase
1278	72.5	3.5	312	2	T33344	hypothetical prote	1351	72	3.4	397	2	B87343	conserved hypothet
1279	72.5	3.5	315	2	AG2361	hypothetical prote	1352	72	3.4	406	2	B35878	class I major hist
1280	72.5	3.5	323	1	PEPLBJ	penicillopepsin (B	1353	72	3.4	416	1	A42879	advanced glycosyla
1281	72.5	3.5	334	2	D83788	UDP-glucose 4-epim	1354	72	3.4	420	2	C71097	hypothetical prote
1282	72.5	3.5	365	1	S76914	translation releas	1355	72	3.4	436	2	T16638	hypothetical prote
1283	72.5	3.5	365	2	JH0537	class I histocompa	1356	72	3.4	456	2	T38221	hypothetical berin
1284	72.5	3.5	366	2	I54430	MHC class I histoc	1357	72	3.4	466	2	JC5897	killer cell inhibi
1285	72.5	3.5	366	2	I61866	MHC HLA-Cw2.2 chai	1358	72	3.4	483	2	S75369	hypothetical prote
1286	72.5	3.5	366	2	I56034	gene HLA-C protein	1359	72	3.4	505	2	T07883	cellulase (EC 3.2.
1287	72.5	3.5	408	2	S76830	phosphoglycerate k	1360	72	3.4	520	2	A71564	hypothetical prote
1288	72.5	3.5	416	1	KIVKGL	A20R protein - vac	1361	72	3.4	539	2	A36187	dihydrolipoamide S
1289	72.5	3.5	426	2	D42519	probable 49.1k pro	1362	72	3.4	569	2	A36187	interleukin-1 rece
1290	72.5	3.5	426	2	T37408	hypothetical prote	1363	72	3.4	580	2	T28725	hypothetical prote
1291	72.5	3.5	432	2	T43476	hypothetical prote	1364	72	3.4	592	2	T43402	probable protein k
1292	72.5	3.5	460	2	T38608	hypothetical prote	1365	72	3.4	622	2	A61197	6-methylsalicylic
1293	72.5	3.5	468	1	VGBEEH	glycoprotein gp13	1366	72	3.4	707	2	T02835	long chain fatty a
1294	72.5	3.5	471	1	PAECA	alkaline phosphata	1367	72	3.4	710	2	T44753	hypothetical prote
1295	72.5	3.5	487	2	A26731	cytochrome P450 2C	1368	72	3.4	733	2	A87168	conserved hypothet
1296	72.5	3.5	497	2	B86485	hypothetical prote	1369	72	3.4	758	2	H75013	hypothetical prote
1297	72.5	3.5	502	2	A83938	lipopolysaccharide	1370	72	3.4	788	2	S17906	hypothetical prote
1298	72.5	3.5	533	2	T34458	hypothetical prote	1371	72	3.4	828	2	E71417	hypothetical prote
1299	72.5	3.5	553	1	H46329	cell fusion glycop	1372	72	3.4	828	2	T22367	hypothetical prote
1300	72.5	3.5	568	2	S57830	glucose-6-phosphat	1373	72	3.4	915	2	T23937	hypothetical prote
1301	72.5	3.5	569	2	S41806	glucose-6-phosphat	1374	72	3.4	974	1	A49714	protein-tyrosine k
1302	72.5	3.5	582	2	A46637	calnexin homolog S	1375	72	3.4	994	2	A32792	Ca2+-transporting
1303	72.5	3.5	605	2	T33913	hypothetical prote	1376	72	3.4	997	1	PWRBSC	Ca2+-transporting
1304	72.5	3.5	612	2	B84936	RNA polymerase sig	1377	72	3.4	997	2	S23181	Ca2+-transporting
1305	72.5	3.5	619	2	A43361	Ets-related transc	1378	72	3.4	997	2	S04651	Ca2+-transporting
1306	72.5	3.5	638	2	T03481	hypothetical prote	1379	72	3.4	997	2	S04651	Ca2+-transporting
1307	72.5	3.5	641	2	G85043	hypothetical prote	1380	72	3.4	997	2	B31982	Ca2+-transporting
1308	72.5	3.5	659	2	G98068	eukaryotic-type se	1381	72	3.4	1042	1	PWRBMC	Ca2+-transporting
1309	72.5	3.5	694	2	G01161	thymopietin alpha	1382	72	3.4	1042	2	A31981	Ca2+-transporting
1310	72.5	3.5	695	2	D71283	probable translati	1383	72	3.4	1042	2	S04652	Ca2+-transporting
1311	72.5	3.5	723	2	T30094	hypothetical prote	1384	72	3.4	1042	2	A33881	Ca2+-transporting
1312	72.5	3.5	745	2	H85048	probable transposo	1385	72	3.4	1043	2	A31982	Ca2+-transporting
1313	72.5	3.5	780	1	S43859	ATPase - Sulfolobu	1386	72	3.4	1062	2	S09834	hypothetical prote
1314	72.5	3.5	820	2	T14879	hypothetical prote	1387	72	3.4	1092	2	JX0312	differentiation-st
1315	72.5	3.5	822	1	IJMSGP	P-cadherin precurs	1388	72	3.4	1135	1	GNVUH7	M polyprotein - Ha
1316	72.5	3.5	845	2	T12537	hypothetical prote	1389	72	3.4	1135	1	GNVUHV	M polyprotein - Ha
1317	72.5	3.5	867	2	AD1856	hypothetical prote	1390	72	3.4	1179	2	T04488	DNA topoisomerase
1318	72.5	3.5	899	2	B75018	hypothetical prote	1391	72	3.4	1210	2	S35548	DNA-directed RNA p
1319	72.5	3.5	980	2	A38523	genome polyprotein	1392	72	3.4	1218	2	AD0837	probable ABC trans
1320	72.5	3.5	1088	1	PFRYGA	platelet-derived g	1393	72	3.4	1218	2	T30293	ABC transport prot
1321	72.5	3.5	1106	2	T31742	hypothetical prote	1394	72	3.4	1289	2	E90098	RNA polymerase III
1322	72.5	3.5	1131	2	T15787	hypothetical prote	1395	72	3.4	1306	2	S25370	MSB2 protein - yea
1323	72.5	3.5	1185	2	T46428	hypothetical prote	1396	72	3.4	1408	2	H69068	cell surface glyco
1324	72.5	3.5	1663	1	C3MS	complement C3 prec	1397	72	3.4	1461	2	E90696	hypothetical prote
1325	72.5	3.5	1707	2	AH2085	two-component hybr	1398	72	3.4	1461	2	A85547	hypothetical prote
1326	72.5	3.5	2271	2	F90073	hypothetical prote	1399	72	3.4	1490	2	S72351	nonstructural poly
1327	72.5	3.5	3283	2	AC1018	large repetitive p	1400	72	3.4	1695	2	A56921	kinesin family pro
1328	72	3.4	111	2	S26256	T-cell receptor be	1401	72	3.4	1774	2	S13178	6-methylsalicylic
1329	72	3.4	111	2	S26255	T-cell receptor be	1402	72	3.4	2090	2	S26058	probable transform
1330	72	3.4	111	2	S09963	Ig kappa chain V-J	1403	72	3.4	2492	1	MNWTD	nonstructural poly
1331	72	3.4	136	2	S36304	T-cell receptor de	1404	72	3.4	2684	2	A96521	protein P21D18.22
1332	72	3.4	138	2	PN0538	Ig heavy chain V r	1405	72	3.4	5188	2	B85547	probable RTX famil
1333	72	3.4	144	2	A27577	T-cell receptor al	1406	72	3.4	5291	2	F90696	hypothetical prote
1334	72	3.4	171	2	S38237	hypothetical prote	1407	72	3.4	101	2	D25733	T-cell receptor al
1335	72	3.4	259	2	F69678	involved in polyke	1408	71.5	3.4	102	2	S29588	Ig kappa chain V r
1336	72	3.4	281	1	S34626	translation elonga	1409	71.5	3.4	112	2	S22891	T-cell receptor al
1337	72	3.4	289	2	S29271	ribonuclease (EC 3	1410	71.5	3.4	113	2	S03410	Ig kappa chain pre
1338	72	3.4	296	2	I46021	Fc-gamma receptor	1411	71.5	3.4	139	1	RWHU7A	T-cell receptor al
1339	72	3.4	333	2	JC7713	ankyrin-repeat pro	1412	71.5	3.4	142	2	S36310	T-cell receptor de
1340	72	3.4	336	2	I49582	CD1.1 - mouse	1413	71.5	3.4	148	2	A32536	T-cell receptor al
1341	72	3.4	350	2	I54308	MHC HLA B71 - huma	1414	71.5	3.4	155	2	S58178	T cell antigen rec
1342	72	3.4	352	2	G81921	hypothetical prote	1415	71.5	3.4	155	2	S71257	major latex protei
1343	72	3.4	354	2	S24437	class I histocompa	1416	71.5	3.4	238	2	B84951	hypothetical prote

1417	71.5	3.4	246	2	PC4397	mucin 3 T10 - huma
1418	71.5	3.4	255	1	S48146	mucin 1 precursor,
1419	71.5	3.4	259	2	S60617	hypothetical prote
1420	71.5	3.4	270	2	G84163	hypothetical prote
1421	71.5	3.4	291	2	JQ1562	hypothetical 33.9K
1422	71.5	3.4	319	2	I39866	microbial serine p
1423	71.5	3.4	329	2	JC5168	UDPGlucose 4-epime
1424	71.5	3.4	337	2	S65022	glucan endo-1,3-be
1425	71.5	3.4	345	2	I68749	MHC class I lympho
1426	71.5	3.4	349	1	E64096	UDPGlucose-hexose-
1427	71.5	3.4	364	2	G64086	glycerophosphodies
1428	71.5	3.4	366	2	I37526	MHC class I histoc
1429	71.5	3.4	366	2	I72113	MHC histocompatibi
1430	71.5	3.4	366	2	I59622	lymphocyte antigen
1431	71.5	3.4	366	2	I38507	MHC class I histoc
1432	71.5	3.4	370	2	A39115	glucan endo-1,3-be
1433	71.5	3.4	380	2	E87729	protein Y23H5A.4 [
1434	71.5	3.4	380	2	T26570	hypothetical prote
1435	71.5	3.4	384	2	A47479	heparin lyase (EC
1436	71.5	3.4	398	1	S45545	GTP cyclohydrolase
1437	71.5	3.4	398	2	H96967	protein containing
1438	71.5	3.4	426	2	T28563	hypothetical prote
1439	71.5	3.4	426	2	C36850	A21R protein - var
1440	71.5	3.4	428	1	AURZOD	glutamate-ammonia
1441	71.5	3.4	436	2	A53568	methylcrotonoyl-Co
1442	71.5	3.4	492	2	T47720	pyruvate kinase-1i
1443	71.5	3.4	528	2	PC4025	intercellular adhe
1444	71.5	3.4	564	2	T42695	hypothetical prote
1445	71.5	3.4	567	2	AF0214	ribulokinase (EC 2
1446	71.5	3.4	570	2	S56132	cellulase (EC 3.2.
1447	71.5	3.4	586	2	T19075	hypothetical prote
1448	71.5	3.4	587	1	A36936	nitrogenase (EC 1.
1449	71.5	3.4	591	2	AB0509	oxaloacetate decar
1450	71.5	3.4	591	2	AB0909	oxaloacetate decar
1451	71.5	3.4	640	1	A55073	transforming prote
1452	71.5	3.4	647	2	AE1054	2',3'-cyclic-nucle
1453	71.5	3.4	668	1	A42908	meprin A (EC 3.4.2
1454	71.5	3.4	687	2	T09051	pepa protein - Pse
1455	71.5	3.4	702	2	E69498	hypothetical prote
1456	71.5	3.4	704	2	I39805	cyclomaltohextrin
1457	71.5	3.4	710	2	A96540	hypothetical prote
1458	71.5	3.4	747	2	B47093	cellulase (EC 3.2.
1459	71.5	3.4	793	2	S34830	kinesin-related pr
1460	71.5	3.4	811	2	PN0689	connectin 1 - chic
1461	71.5	3.4	825	2	A59296	alpha-L-arabinofur
1462	71.5	3.4	828	2	S52393	beta-galactosidase
1463	71.5	3.4	857	2	T04208	probable anthranil
1464	71.5	3.4	976	1	URRTAP	peptidylglycine mo
1465	71.5	3.4	987	2	H81722	polymorphic membra
1466	71.5	3.4	1005	1	P1VXPJ	RNA 1 protein - pe
1467	71.5	3.4	1025	2	S34839	collagen alpha 1(V
1468	71.5	3.4	1044	2	E86613	ribonucleoside red
1469	71.5	3.4	1044	2	A72010	ribonucleoside-dip
1470	71.5	3.4	1117	2	S63399	probable membrane
1471	71.5	3.4	1137	2	B90734	probable host spec
1472	71.5	3.4	1138	2	D85584	probable tail comp
1473	71.5	3.4	1179	2	C36792	hypothetical prote
1474	71.5	3.4	1226	2	JC7503	protein-tyrosine-p
1475	71.5	3.4	1358	2	T22695	hypothetical prote
1476	71.5	3.4	1441	2	A86685	prophage pil prote
1477	71.5	3.4	1490	2	JC5145	DNA (cytosine-5-)-
1478	71.5	3.4	1582	2	AC1153	adhesin homolog 1m
1479	71.5	3.4	1612	2	AB1347	probable peptidogl
1480	71.5	3.4	1680	2	T41628	probable transcrip
1481	71.5	3.4	1815	2	B95942	conserved hypotet
1482	71.5	3.4	1939	2	D97316	probable S-layer p
1483	71.5	3.4	1946	2	AC2141	serine/threonine k
1484	71.5	3.4	2242	2	A57541	pyrimidine synthes
1485	71.5	3.4	2332	1	GNNYF	genome polyprotein
1486	71.5	3.4	3131	2	S39842	enniatin synthetas
1487	71.5	3.4	3191	2	T22945	hypothetical prote
1488	71.5	3.4	6359	2	T31679	bacitracin synthe
1489	71	3.4	87	2	PH1082	Ig light chain V r

1490	71	3.4	98	2	S26911	Ig heavy chain V r
1491	71	3.4	115	1	KVMSL7	Ig kappa chain pre
1492	71	3.4	123	2	S70243	hypothetical prote
1493	71	3.4	166	2	PL0012	Ig heavy chain pre
1494	71	3.4	180	2	G69222	molybdenum formylm
1495	71	3.4	223	2	T33194	hypothetical prote
1496	71	3.4	254	2	S48547	probable membrane
1497	71	3.4	270	2	T03635	placid-lipid-asso
1498	71	3.4	287	2	E69901	cell wall-binding
1499	71	3.4	321	2	AC0821	probable exported
1500	71	3.4	336	2	C27658	pregnancy-specific

ALIGNMENTS

```

RESULT 1
S56749
functional adhesion molecule precursor - human
N:Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: A59406; S56749
R:Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A:Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A:Reference number: A59406; MUID:99323940; PMID:10395639
A:Accession: A59406
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <OZA>
A:Cross-references: UNIPROT:Q9Y624; GB:AAD42050; NID:G5326797; PIDN:AAD42050.1
R:Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A:Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of
A:Reference number: S56749; MUID:95374438; PMID:7646439
A:Accession: S56749
A:Molecule type: protein
A:Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXIYLNXY','LT',206,'X'
A>Note: the order of the peptides other than the amino terminus was not determined
C:Genetics:
A:Gene: JAM
C:Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-299/Product: functional adhesion molecule #status predicted <MAT>

Query Match      8.5%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 3.5e-06;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY      1 MGILLGLLLGLTLTVDTYGRPILEVPESVTGPMWKGDVNLCTYDPLQGYTVLVKWLVR 60
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      17 LAILLCSLALGSVTVHS-SEDEVRIIPEN-----NPVKLSCAV---SGFSSPRVEW---- 62

QY      61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHK-----VPGDVSLQLSTLEMDRSHYTC 115
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      63 -----KFDQGDTRRLVCYNKKITASYEDRVTFPLPTGITEFKSVTRE--DTGYTCMV 111

QY      116 TWQTPDGNQVVRDKITELAVQKLSVSKPTVTGSGYGFVPGMRISLQCAR-GSPPI 174
      :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      112 SEEGGNSYGEVKKLIVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEQDGSPPSE 163

QY      175 YIWK----QQTN-----NOEPIKAVTLSTLLFKPAVIADSGSYFCTAKGVGSEQH 222
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      164 YTFPKDGIWPTNPKSTRAFSNSSVYLNPTTGELVFDPLSASDTGEYSCEARNGYGTPT 223

QY      223 SDIVK 227
      ||:||||:
Db      224 SNAVR 228

RESULT 2
I38346
```

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elastic titin - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
R/Accession: I38346
R/Labell, S.; Kolmerer, B.
Science 270, 293-296, 1995
A>Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A/Reference number: A57430; MUID:96026330; PMID:7569978
A/Accession: I38346
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-7962 <RES>
C/Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
A/Gene: GDB:TIN
A/Cross-references: GDB:I27867; OMIM:188840
A/Map position: 2q31-q31

Query Match      8.5%; Score 178; DB 2; Length 7962;
Best Local Similarity   24.2%; Pred. No. 0.00025;
Matches    102; Conservative     56; Mismatches    169; Indels     94; Gaps     20;

OY       16 DTVGRPILEVPES-VTGPWKGDVNLP---CTYPDLOGYTQLVKW-----LVQRGSDP 64
           |||::|||:|||::|||::|||::|||::|||::|||::|||::|||
Db        860 DSSGALIVQEPPSFVTKEGSKDV-LPGSAVLCKSTFGOSTPLTIKRWFKGNKEIWSGSscy 918
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY         65 VTIFLRDSSGDHIQAAYQGRHLVSHKVPGDVDSLQLEMLEMDDRSHYTEAVTQTDPG-- 122
           :||:IT-----XEALESSELEYLVKTSDSGTYTCkVS-NVAGGVE 953
          919 IT-----XEALESSELEYLVKTSDSGTYTCkVS-NVAGGVE 953

OY       123 ---NQVRDKITELRVOKLSVSKPTVTTSgyGFtvpQGMRISLoQQARGSPPIsiwyk 179
           |::||:|||||::|||::|||::|||::|||::|||::|||::|||
Db        954 CSANLFvkePAT-FveklePSQ-----LLKGdAToLaCKkvGTgTPPiKITwFA 1000
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY       180 QOTNNQEPik----VALTLTLFKAVIDSGSYfctaKgQVGSeQHsdIyKFvvkdss 234
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       1001 NDREIKESSKHrMSfvESTAvILRLTDvgIEDSgefwcEaQNAGSDHCssiiv--lvkesP 1058
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY       235 ----KLTKTEAPRTWTYPYLkaISTVkQSwdMTDMdyLGETSagPgksLvPfaiI 288
           |::||:|||||::|||::|||::|||::|||::|||::|||::|||
Db       1059 YFTKEFPievlKeYdvMLlaEvAgTpPFETw-----fkDNtiRSGrkyktFIQD 1110
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY       289 LIISLCm-vftMayImLCRKtsQOEhvyEARAhAREAn-----DSGETWR--VAIf 339
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       1111 HLvsLIqlkfvaADAGEYCrvTNevGsSiCSARvtlReppsfIkIEStslRGTAaf 1170
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY       340 ASGCSSDEPTSQNLgnNSDePCIGeEQIIAQINGNYArL-lDTvPlDYEFLaTeGKSv 398
           ::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db       1171 qAtLKgsLPitvTWlkD-sDE--ItEDNIrmTFENNVASLYlsGIevKh-----DGKYV 1222
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY       399 C 399
           |
Db       1223 c 1223

RESULT 3
JC7780
cox sackie- and adenovirus receptor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C/Accession: JC7780
R/Theelen, L.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A>Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptc
A/Reference number: JC7780
A/Contents: Liver
A/Accession: JC7780
A/Molecule type: mRNA
A/Residues: 1-365 <THO>
C/Cross-references: UNIPROT:Q8WMV3; GB:AY033651
C/Comment: This protein serves as the primary adenoviral attachment site on bovine cells
```

QY	1	MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGD-VNLPCITY-----DPLQGYTQV	52
Db	1	MELLIRFLLLCGVADFTRGLSI-TTPEQMIEKAKGETAYLPCKFTLGEDDQGPLD-----	54
QY	53	LVKWLNVGRGS----DPVTIFLRDSSGGDHIOAKYQ---GRLVSHK--VPGDVSLLQLSTL	103
Db	55	-IEWLSPADNOQKVDQVIILY---SGDKYIDDYYQDLKGRVHFTSNLKSGDASINVTNL	110
QY	104	EMDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTGSGYFTVPQ---GM	159
Db	111	QLSDIGTYQCKVKA PGVGNK-----KIQLTVLVP----SGIRCYVDGSEEIGN	156
QY	160	RISLQCCQAR-GSPPISYIWKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAKG	215
Db	157	DFKLKCEPKEGSLPLRYEWQKLSDSQKLPSTWLPMTSPVISVKMSAEYSGYTCTVRN	216
QY	216	QVGEQHSDDIVKRVKDSKLLKTKTEAPTMTYPLKATSTVKQSWDWTDDMDGYLGETS	275
Db	217	RVGSDQ-----CLRLDVPVPSNR-----AGTI	239
QY	276	AGPGKSLPVFAIILLISLCMVFTMAYIMLCRKTSQGEHVEAARAH	323
Db	240	AG-----AVIGTLLALVLIALIVF-----CCHKRREKEKEVHH	275

RESULT 4

S19247

cell adhesion protein Gpi60-Dtrk - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004

C;Accession: S19247

R;Pulido, D.; Campuzano, S.; Koda, T.; Modellell, J.; Barbacid, M.

EMBO J. 11, 391-404, 1992

A;Title: Dtrk, a Drosophila gene related to the trk family of neurotrophin receptors, en

A;Reference number: S19247; MUID:92164624; PMID:1371458

A;Accession: S19247

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1033 <PUL>

A;Cross-references: UNIPROT:Q24327; EMBL:X63453; NID:g7883; PIDN:CAA45053.1; PID:g7884

C;Genetics:

A;Gene: FlyBase:Tk48D

A;Cross-references: FlyBase:FBgn0004839

C;Superfamily: protein kinase homology

C;Keywords: ATP

F;690-1028/Domain: protein kinase homology <KIN>

F;698-706/Region: protein kinase ATP-binding motif

QY	22	ILEVPES--VTGPMKGDVNLPC---TYDPLQGYTQVLVKWLNVGRSDPVTIFLRDSSG	74
Db	370	ILEVIEQLKFVPQPTSKNLELDAAVAKVCKAQGTPTPQVQWV--RDGENTTL-----P	421
QY	75	DHIQAKYQGRLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELR	134
Db	422	DHVE-----VDANGTLIFRNVNSEHRGNYTCLATNSQGQINATV--AINVV	466
QY	135	VQKLSVSK--PIVTTGSGYGFVTPQGMKRLSLQCCQARGSPPISYIWK-----QQTNNQ	186
Db	467	TPKFSVPVPVGPIETSEQG-----TVVMHCQAIGDPKPTIQMDKDLKYLSENNTDRE	517
QY	187	PIKATLSTLLFKPAVIADSGSYFCTAKQGVGEQHSDIVKRVVVDSSKLLKTKTEAPTT	246
Db	518	RFRFLNGTLEIRNVQVEDEGSYGCTIGNSAGLKRED--VQLVVK-----	560
QY	247	MTYPLKATSTVKQSWDWTDDMDGYLGTSAGPGKSLPVFAIILLISLCMVFTMAYIML	306

Db 561 -----TTGDGFAPEESGDFLVTRAVLITMTVALAYIVLVGIMLN 602

Qy 307 CRKTSQOEHVYEAAAHAREA--NDSGETMRVAIFASGSSDEPTSQNLGNYSDEPTIG 364

Db 603 CR-----YRQARKARLND-----LSTKEAGGDQPDIDAGNGKSGEQEPCLIS 643

Qy 365 QEY 367

Db 644 KQH 646

RESULT 5

B49120

protein-tyrosine kinase (EC 2.7.1.112) dtk2 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C:Accession: B49120; S18010

R:Shishido, E.; Higashijima, S.; Emori, Y.; Saigo, K.

Development 117, 751-761, 1993

A:Title: Two FGF receptor homologues of Drosophila: one is expressed in mesodermal primord

A:Reference number: A49120; MUID:93321617; PMID:8330538

A:Accession: B49120

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-1052 <SHI>

A:Cross-references: UNIPROT:Q09147; GB:X74031; GB:S63797; NID:g397600; PIDN:CAA52190.1;

A:Experimental source: pupa

A>Note: sequence extracted from NCBI backbone (NCBIN:135151, NCBIP:135153)

R:Shishido, E.; Emori, Y.; Saigo, K.

FEBS Lett. 289, 235-238, 1991

A:Title: Identification of seven novel protein-tyrosine kinase genes of Drosophila by th

A:Reference number: S17552; MUID:92008631; PMID:1915852

A:Accession: S18010

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 869-922 <SH2>

C:Genetics:

A:Gene: FlyBase:tbl; dtk2

A:Cross-references: FlyBase:FBgn0005592

C:Superfamily: protein kinase homology

C:Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein k

F:710-1003/Domain: protein kinase homology <KIN>

F:718-726/Region: protein kinase ATP-binding motif

Query Match 6.8%; Score 143.5; DB 2; length 1052;

Best Local Similarity 23.4%; Pred. No. 0.0082;

Matches 71; Conservative 44; Mismatches 119; Indels 69; Gaps 14;

Qy 16 DTYGRPILE-----VPESYTGPMKGDVNLPT-LOGYTVQLVKMLVQSGSDP 64

Db 130 DLFFQPLNESRLKLQPLPKTVQRTAGLFLQNCSPMDPAKG---VNISWL----- 179

Qy 65 VTFLRDSSGDHIQQAQYQGRLVHSHKVPGDVSLQLSTLEMDDRSHTYCEVTWQTPDGNQ 124

Db 180 -----HIDTQILGGRRIKLK--RMSLTVGQLQPEDAGSYHCELCVE----QD 221

Qy 125 VVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRIISLQCCARGS--PISYIWKQ 181

Db 222 CQRSNPTQLEVISRKHTVPMKPGYPRNTSIALGDNVSIIECLIEDSALPKITWL-HKGN 280

Qy 182 TNN-----QEPKIVATISLLLEKPAVI-----ADSGSYFCTAKQGVSEQH 222

Db 281 ADNIDDLLQRLREQSQLPVDVTRLITRMDPEQVLRLGNVLMEDEGWYICIAENQVGRIVA 340

Qy 223 SDIVKRVVKDSSKLKTKTEAPTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSL 282

Db 341 ASYVDLVSPSDTTTTRTTT--TTVASPIPTASTGEDND---DVENPAADASGAVGP-- 393

Qy 283 PVF 285

Db 394 PVF 396

RESULT 6

S18252

heparan sulfate proteoglycan - mouse

N:Alternate names: perlecan

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 12-Jul-2004

C:Accession: S18252; A31917; B31917; S66460

R:Noonan, D.M.; Fulle, A.; Valente, P.; Cal, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha

J. Biol. Chem. 266, 22939-22947, 1991

A:Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogl

adhesion molecule.

A:Reference number: S18252; MUID:92078153; PMID:1744087

A:Accession: S18252

A:Molecule type: mRNA

A:Residues: 1-3707 <NOO>

A:Cross-references: UNIPROT:Q05793; EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g2002

R:Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Ha

J. Biol. Chem. 263, 16379-16387, 1988

A:Title: Identification of cDNA clones encoding different domains of the basement membra

A:Reference number: A92680; MUID:89034110; PMID:2972708

A:Accession: A31917

A:Molecule type: mRNA

A:Residues: 940-1601 <NO2>

A:Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253

A:Accession: B31917

A:Molecule type: mRNA

A:Residues: 1870-2600 <NO3>

A:Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301

R:Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.

Eur. J. Biochem. 231, 551-556, 1995

A:Title: Structural properties of recombinant domain III-3 of perlecan containing a glob

A:Reference number: S66460; MUID:95377282; PMID:7649154

A:Accession: S66460

A:Molecule type: protein

A:Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>

C:Keywords: glycoprotein

F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F:764-811/Domain: laminin-type EGF-like homology <LEG>

F:1159-1206/Domain: laminin-type EGF-like homology <LEG7>

F:1563-1610/Domain: laminin-type EGF-like homology <EG7>

F:1613-1668/Domain: laminin-type EGF-like homology <LEG8>

F:3163-3198/Domain: EGF homology <EGF>

F:3270-3423/Domain: laminin G repeat homology <LG2>

F:3464-3492/Domain: EGF homology <EGF7>

F:1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.6%; Score 139.5; DB 2; length 3707;

Best Local Similarity 25.1%; Pred. No. 0.083;

Matches 66; Conservative 31; Mismatches 105; Indels 61; Gaps 14;

Qy 13 LTVDT----YGRPILEVPESVTGPMKGDVNLPTTYDPLQGYTVQLVKMLVQSGSDPVITF 68

Db 2521 LIVDTGTVAAPGTPQVQVEES-----ELTLEA-----GHTATL--HCSATGNPPPT-- 2563

Qy 69 IRDSSGDHIQQAQYQGRLVHSHKVPGDVSLQLSTLEMDDRSHTYCEVTWQTPDGNQVVRD 128

Db 2564 -----IHWSKLRAPLPMQHRILEGN-TLVIPRVAQODSGQYICNAT-----NSAGHT 2608

Qy 129 KITELRVQKLSVSKPTVTGSGYGFVTPQ-----GMRISLQCCARGSPPISYIWKQQT 182

Db 2609 EATVV-----LHVESPP-----YATIIPEHTSAQPGNLVQLQCLAHGTPPLTYQW--SLV 2656

Qy 183 NNOEPIKIVATLSTLL-FKPAVIADSGSYFCTAKQGVSEQHSDIVKRVKDSKSLKTKT 241

Db 2657 GGVLPKAVVRNQLRLRLEPTVPEDSGRYRCQVSNRVGSAA--AFAQVLVQGSSSSNLEPDS 2714

Qy 242 ----EAPTMTYPLKATSTVKQS 260

Db 2715 IPGSGTPTVQVTPQLETRNIGAS 2737

RESULT 7
PFHUGB
platelet-derived growth factor receptor beta precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A28206; A31195; A38268; A31925; B31925; C31925
R;Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988
A;Title: Cloning and expression of a cDNA coding for the human platelet-derived growth f
A;Reference number: A28206; MUID:88217915; PMID:2835772
A;Accession: A28206
A;Molecule type: mRNA
A;Residues: 1-1106 <GRO>
A;Cross-references: UNIPROT:P09619; GB:J03278; NID:g189731; PIDN:AAA60049.1; PID:g189732
R;Claesson-Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek, B.; Oestman, A.; Bet
Mol. Cell. Biol. 8, 3476-3486, 1988
A;Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) re
A;Reference number: A31195; MUID:89096941; PMID:2850496
A;Accession: A31195
A;Molecule type: mRNA
A;Residues: 1-240,'D',242-1106 <CLA>
A;Cross-references: GB:M21616; NID:g189729; PIDN:AAA36427.1; PID:g189730
R;Partanen, J.; Maekela, T.P.; Altalo, R.; Lehtelaaho, H.; Altalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: A38268
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 828-884 <PAR>
R;Roberts, W.M.; Look, A.T.; Rousset, M.F.; Sherr, C.J.
Cell 55, 655-661, 1988
A;Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.
A;Reference number: A90908; MUID:89028677; PMID:2846185
A;Accession: A31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 676-727 <ROB>
A;Accession: B31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 901-982 <RO2>
A;Accession: C31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1047-1106 <RO3>
C;Comment: The extracellular domain is predicted to include five immunoglobulin-like dom
C;Genetics:
A;Gene: GDB:PDGFRB
A;Cross-references: GDB:120710; OMIM:173410
A;Map position: 5q31-5q32
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-1106/Product: platelet-derived growth factor receptor beta #status predicted <MAT>
F;33-531/Domain: extracellular #status predicted <EXT>
F;47-102/Domain: immunoglobulin homology <IMM1>
F;142-192/Domain: immunoglobulin homology <IMM2>
F;228-293/Domain: immunoglobulin homology <IMM3>
F;429-510/Domain: immunoglobulin homology <IMM4>
F;532-555/Domain: transmembrane #status predicted <TM>
F;556-1106/Domain: intracellular #status predicted <INT>
F;598-965/Domain: protein kinase ATP-binding motif
F;606-614/Region: protein kinase ATP-binding motif
F;45, 89, 103, 215, 230, 292, 307, 354, 371, 468, 479/Binding site: carbohydrate (Asn) (covalent)
F;54-100, 149-190, 235-291, 436-508/Disulfide bonds: #status predicted
F;634/Active site: Lys #status predicted
F;857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Matches 85; Conservative 59; Mismatches 126; Indels 162; Gaps 19;
QY 23 LEVPEVSVTGPW-----KGDVNLPCITYDPLQGYTVLWKVLVQRGSDPVTIFLRDSSG 74
: : | | | | | | | | | : : : :
Db 145 ITIPCRVTDPLVTVLHEKKGDVALPVPYDHQRFSGI----- 182
QY 75 DHIQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHTCEVTWQTPDGNQVVRDKITELR 134
: : : : | | | | : : : :
Db 183 -----FEDRSYICKTTIGD-----REVSDAYV-----VYRLQ 210
QY 135 VQKLSVSKPTVTTGSGYFTVPQGMRIQLQCARGPSPIISYIW-YKQQTNNQ--EPIKVA 191
: : | | | | | | | | | : : : : : : : :
Db 211 VSSINVSNAVQT-----VVRQGENITLMCIYIGNEVNVFEMTYPRKESGRIVEPVTDF 264
QY 192 TL-----STLFKPAVIADSGSYFCTAKGQVSGEQHSDIVKPVVKDSSKLLKTKEAP 244
: : | | | | | | | | | : : : : : : : :
Db 265 LIDMPYHIRSILHIPSAALEDSGTYTCNVTESVNDHQDEKAINITVESG-YVRLGVEVG 323
QY 245 TMTYPLKATSTVKQSWD-----WTTMDGYLGFTSAGPGKSLPVFAILLIISLCM 296
| : : : : : : : : : : : : : : : : : :
Db 324 TLQFAELHRSRTLQVVEAYPPPTVLWFKD-NRTLGDSSAGE-----IALSTR 370
QY 297 VFTMYAI---MLCRKTSQOEH-----VYEARAHAAREA 327
| : : : : : : : : : : : : : : : : : :
Db 371 NVSETRYVSELTLLVRKVAEAGHYTMRAFHDEAEVQLSFQLQINVPVRVLESESHP--- 427
QY 328 NDSGE-TMRVA-----IFASGC-----SSDEPTSQNLGNYSDEP 361
| | | | | : | : | : | : | : | : | :
Db 428 -DSGEQTVRCRGRGMPQNIWISACRDLKRCPRELPPTLLGNSSSEESQLETVTYWEE 486
QY 362 CIGQEQYIIAQI 373
| : : : : : : : : : : : : : : : : : :
Db 487 ---QEFVSTL 495

RESULT 8
PN0568
connectin 3B - chicken (fragment)
N;Alternate names: Cn3B protein
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: PN0568
R;Maruyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanzawa, N.; Nakauchi, Y.; Kimura, S.;
Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993
A;Title: A novel domain sequence of connectin localized at the 1 band of skeletal muscle
A;Reference number: PN0568; MUID:93356802; PMID:8352787
A;Accession: PN0568
A;Molecule type: mRNA
A;Residues: 1-1323 <MAR>
A;Cross-references: UNIPROT:O08476; DDBJ:D16541; NID:g391629; PID:d1004495; PID:g391630
A;Experimental source: skeletal muscle
C;Comment: This protein string-like single molecule spans from the Z line to the M line
Query Match 6.6%; Score 138.5; DB 2; Length 1323;
Best Local Similarity 21.4%; Pred. No. 0.026;
Matches 61; Conservative 38; Mismatches 117; Indels 69; Gaps 10;
QY 22 LLEVESV---TGPWKGDVNLPCITYDPLQGYTVLWKVLVQRGSDPVTIFLRDSSGDHIQ 78
| | | | | : : : | | | : : : : : : :
Db 143 ILIIPNSKLEDQGYSCHIEENDSGQDNCHGALTILEPPYFVTPLPEPVQYTVGSAASLQ 202
QY 79 QAK-----YQG-----RLVSHKYPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
| : : : : : : : : : : : : : : : : : :
Db 203 VAGTPEMIVSWYKGDTRLRGTAIVKMHFKQY---ATLVFSQVDSDDSGEYICKVENTVG 259
QY 121 DGNQ-----VVRDKITELRVQKLSVSKPTVTTGSGYFTVPQGMRIQLQCARGPSPIISY 175
: : | | | | | : : : | | | : : : : : : :
Db 260 EATSSSLTTVQERKLPPSFTRLRDVHETV-----GLPVTFCGIAGSEPIEV 307
QY 176 IWYKQQTNNQEPKIVAT--LSTLLFKPAVIADS---GSYFCTAKGQVSGEQHSDIVKVV 230
| : | : | : | : | : | : | : | : | : | :
Db 308 SWFKDNVRVKEDVNVHTSFIDNVAIQLKTPKSLMGQYCTASNAIGT-----A 357

C;Accession: A42632

R; Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.

Science 256, 638-644, 1992

A/Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plasticity
A/Reference number: A42633
WITD: 03263005
DWID: 1506176

A;Reference number: A42632; MUID:92263095; PMID:1585176

A; Accession: A42632

A; Status: preliminary; not compared with conceptual translation

A; molecule type: nucleic acid

A;ResIdues: 1-932 <MAY>

A; Cross-references: UNIPROT:Q9TWA6

A; Experimental source: CNS

A;Note: sequence extracted from NCBI backbone (NCBIP:101342)

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match 6.3%; Score 132.5; DB 2; Length 932;

Best Local Similarity 20.7%; Pred. No. 0.049;

Matches 54; Conservative 31; Mismatches 63; Indels 113; Gaps 10;

QY 104 EMDRSHYTCV-----TWQTPDGNQVVRDKITELRVQKLSVSKPT-----VTTGSG 150

Db 230 KVGDEVKITCQATGVPPTTYQFKKGDVMTDEMWNNGVLTINPLKTTDQATYTCIATNKG 289

QY 151 YGFT-----VP-----QGMRISLQCGARGSPISYW----- 177

Db 290 -GFAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAKGDPEPSVIWKDGPQASTD 348

QY 178 -----YKQNTNQEPIKVA TLST-LLEKPAVIADSGSYCTAKGQVGSEQHS D I V K F 228

Db 349 GIYNKGPTYEKVGSNDMEECTVAQHMTFKPVITYQDAGTYICTAFSLVGSANKT--VKL 406

QY 229 VVK-----DSSKLLKTKT 241

Db 407 TVQYKPNEDTDFKEREFEGWRGKANLTCQANANPVATIEWYMPDAENPDDYSKAVRIPN 466

QY 242 EAPITMYPLKATSTVKQSD 262

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Db      467 EAPYTI-----NMLQKWD 479

```

Search completed: March 2, 2005, 15:22:22
Job time : 42 secs

Job time : 42 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2005, 15:20:17 ; Search time 66 Seconds
(without alignments)
3095.751 Million cell updates/sec

Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILLGLLLGLHLYVTYGR.....LDDTVPLDYFLATEGKSVK 399

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2098	100.0	399	2 Q9Y279	Q9Y279 homo sapien
2	1688	80.5	321	2 Q6UX14	Q6UX14 homo sapien
3	840	40.0	280	2 Q8OWA3	Q8OWA3 mus musculu
4	178.5	8.5	299	1 JAM1_HUMAN	Q9Y624 homo sapien
5	178	8.5	7962	2 Q10465	Q10465 homo sapien
6	178	8.5	34350	2 Q8WZ42	Q8WZ42 homo sapien
7	177	8.4	319	1 A33_HUMAN	Q99795 homo sapien
8	170.5	8.1	292	2 Q66T72	Q66T72 brachydanio
9	170	8.1	365	2 Q8WMV3	Q8WMV3 bos taurus
10	169.5	8.1	298	1 JAM1_BOVIN	Q9X566 bos taurus
11	168	8.0	300	2 Q8VC39	Q8VC39 mus musculu
12	168	8.0	319	2 Q9TUV9	Q9TUV9 sus scrofa
13	167.5	8.0	319	2 Q9TUV8	Q9TUV8 canis famil
14	167	8.0	300	1 JAM1_MOUSE	Q88792 mus musculu
15	167	8.0	300	2 Q9UTH1	Q9UTH1 rattus norv
16	165	7.9	335	2 Q9PWR4	Q9PWR4 gallus gall
17	163	7.8	335	2 Q9YGH1	Q9YGH1 gallus gall
18	161	7.7	319	1 A33_MOUSE	Q9JKA5 mus musculu
19	160	7.6	291	2 Q66T15	Q66T15 xenopus tro
20	159	7.6	332	2 Q6P359	Q6P359 xenopus tro
21	159	7.6	344	2 Q9UKV4	Q9UKV4 homo sapien
22	159	7.6	365	2 CXAR_HUMAN	Q9H6B4 homo sapien
23	158.5	7.6	373	2 Q9H6B4	Q9H6B4 homo sapien
24	157	7.5	335	2 Q9YGV5	Q9YGV5 gallus gall
25	156.5	7.5	5516	2 Q7Z248	Q7Z248 brachydanio
26	156	7.4	289	2 Q7ZWT0	Q7ZWT0 xenopus lae
27	154.5	7.4	512	2 Q96DN8	Q96DN8 homo sapien
28	154.5	7.4	5636	2 Q96RW7	Q96RW7 homo sapien
29	152.5	7.3	372	2 Q8K1G0	Q8K1G0 rattus norv
30	151	7.2	390	2 Q9H1X9	Q9H1X9 homo sapien
31	150	7.1	1395	2 Q44924	Q44924 drosophila

32	149.5	7.1	344	2 Q9R067	Q9R067 rattus norv
33	149.5	7.1	358	2 Q9R066	Q9R066 rattus norv
34	149	7.1	373	2 Q920S5	Q920S5 mus musculu
35	149	7.1	1395	2 Q7KVK3	Q7KVK3 drosophila
36	149	7.1	1429	2 Q9W213	Q9W213 drosophila
37	148	7.1	373	2 Q8R373	Q8R373 mus musculu
38	145.5	6.9	1271	2 Q6U714	Q6U714 brachydanio
39	145.5	6.9	3410	2 Q7TN00	Q7TN00 rattus norv
40	145	6.9	3950	2 Q7YRF5	Q7YRF5 canis famil
41	144.5	6.9	537	2 Q7PSJ8	Q7PSJ8 anopheles g
42	144.5	6.9	1033	2 Q24327	Q24327 drosophila
43	144.5	6.9	1033	2 Q9V643	Q9V643 drosophila
44	143.5	6.8	403	2 Q9VP08	Q9VP08 drosophila
45	143.5	6.8	1052	1 FGR2_DROME	Q09147 drosophila
46	143.5	6.8	1316	2 Q7QET6	Q7QET6 anopheles g
47	143	6.8	448	2 Q8IGAS	Q8IGAS drosophila
48	142.5	6.8	372	2 Q90Y50	Q90Y50 brachydanio
49	142.5	6.8	396	2 Q99N28	Q99N28 m neectin-1t
50	142.5	6.8	523	2 Q80ZE2	Q80ZE2 mus musculu
51	142.5	6.8	1117	2 Q6P1C6	Q6P1C6 mus musculu
52	142	6.8	714	2 Q6ZPE6	Q6ZPE6 mus musculu
53	142	6.8	4071	2 Q6KDZ1	Q6KDZ1 gallus gall
54	141.5	6.7	305	2 Q8VIM2	Q8VIM2 mus musculu
55	141	6.7	1052	2 Q9VUC8	Q9VUC8 drosophila
56	140.5	6.7	352	2 Q91W66	Q91W66 mus musculu
57	140.5	6.7	359	1 LACH_DROME	Q24372 drosophila
58	140.5	6.7	359	2 Q9V6C2	Q9V6C2 drosophila
59	140.5	6.7	365	1 CXAR_MOUSE	P97792 mus musculu
60	140.5	6.7	365	2 Q9DBJ8	Q9DBJ8 mus musculu
61	140.5	6.7	397	2 Q6XRC3	Q6XRC3 homo sapien
62	140	6.7	308	2 Q68EV1	Q68EV1 xenopus lae
63	140	6.7	332	2 Q64U03	Q64U03 xenopus tro
64	140	6.7	1662	2 Q7QIV4	Q7QIV4 anopheles g
65	139.5	6.6	413	2 Q6ZNI1	Q6ZNI1 homo sapien
66	139.5	6.6	3707	1 PGBM_MOUSE	Q05793 mus musculu
67	139	6.6	330	2 P97269	P97269 cavia porce
68	139	6.6	377	2 Q9VQY0	Q9VQY0 drosophila
69	139	6.6	1106	1 FGDR_HUMAN	P09619 homo sapien
70	139	6.6	1479	2 Q7KQTS	Q7KQTS drosophila
71	139	6.6	1482	2 Q9V4Y0	Q9V4Y0 drosophila
72	138.5	6.6	310	1 JAM3_HUMAN	Q9XB67 homo sapien
73	138.5	6.6	310	2 Q9DB87	Q9DB87 mus musculu
74	138.5	6.6	423	2 Q8BU57	Q8BU57 mus musculu
75	138.5	6.6	569	1 SILF_MOUSE	Q920G3 mus musculu
76	138.5	6.6	1323	2 Q08476	Q08476 gallus gall
77	138.5	6.6	4162	2 Q98918	Q98918 gallus gall
78	138	6.6	285	2 Q9D780	Q9D780 mus musculu
79	138	6.6	298	2 Q804R4	Q804R4 brachydanio
80	138	6.6	360	1 HPL3_HUMAN	Q96S86 homo sapien
81	138	6.6	463	2 Q6NJ72	Q6NJ72 xenopus lae
82	138	6.6	697	2 Q8NC72	Q8NC72 homo sapien
83	138	6.6	1059	2 Q6UX17	Q6UX17 homo sapien
84	138	6.6	1119	2 Q6UXM1	Q6UXM1 homo sapien
85	138	6.6	2022	2 Q7KQ05	Q7KQ05 drosophila
86	137.5	6.6	309	2 Q96FL1	Q96FL1 homo sapien
87	137.5	6.6	310	2 Q9D1M9	Q9D1M9 mus musculu
88	137.5	6.6	310	2 Q9EPK4	Q9EPK4 m junctiona
89	137.5	6.6	461	2 Q13854	Q13854 homo sapien
90	137.5	6.6	749	2 Q967D9	Q967D9 drosophila
91	137.5	6.6	902	2 Q81Q17	Q81Q17 drosophila
92	137.5	6.6	903	2 Q967D8	Q967D8 drosophila
93	137.5	6.6	903	2 Q9VQY1	Q9VQY1 drosophila
94	137.5	6.6	1508	2 Q6NR34	Q6NR34 drosophila
95	137.5	6.6	1508	2 Q9VQY2	Q9VQY2 drosophila
96	137.5	6.6	1531	2 Q967D7	Q967D7 drosophila
97	137	6.5	344	2 Q9VY33	Q9VY33 drosophila
98	137	6.5	398	2 Q8N126	Q8N126 homo sapien
99	137	6.5	432	2 Q9UJPI	Q9UJPI homo sapien
100	137	6.5	450	2 Q6UX10	Q6UX10 homo sapien
101	137	6.5	2016	2 Q8MKM6	Q8MKM6 drosophila
102	137	6.5	2016	2 Q8MKM7	Q8MKM7 drosophila
103	137	6.5	2016	2 Q9NEA1	Q9NEA1 drosophila
104	137	6.5	2019	2 Q8MKM8	Q8MKM8 drosophila

105	137	6.5	2828	2	Q9NR99	Q9nr99 homo sapien
106	136.5	6.5	394	2	Q7ZXX1	Q7zxx1 xenopus lae
107	136.5	6.5	487	2	Q7T2H2	Q7t2h2 gallus gall
108	136.5	6.5	1624	2	Q63ZG4	Q63zg4 xenopus lae
109	136.5	6.5	1827	2	Q9VSG5	Q9vsg5 drosophila
110	136	6.5	283	2	Q9VT76	Q9vt76 drosophila
111	136	6.5	316	2	Q7TPB4	Q7tpb4 rattus norv
112	136	6.5	584	2	Q9Y3Y8	Q9y3y8 homo sapien
113	136	6.5	1431	2	Q80U60	Q80u60 mus musculu
114	135.5	6.5	298	2	Q8C5K9	Q8c5k9 mus musculu
115	135.5	6.5	439	2	Q57349	Q57349 gallus gall
116	135.5	6.5	632	2	Q6ZRK5	Q6zrk5 homo sapien
117	135	6.4	394	2	Q925F2	Q925f2 mus musculu
118	135	6.4	838	2	Q90YM1	Q90ym1 brachydanio
119	135	6.4	1235	2	Q7Q0S7	Q7q0s7 anopheles g
120	135	6.4	2013	2	Q8VHZ8	Q8vhz8 rattus norv
121	135	6.4	2013	2	Q9ERC8	Q9erc8 mus musculu
122	134.5	6.4	298	2	Q8CE95	Q8ce95 mus musculu
123	134.5	6.4	303	2	Q7ZXR4	Q7zxr4 xenopus lae
124	134.5	6.4	2597	2	Q6WRH9	Q6wrh9 rattus norv
125	134	6.4	442	2	Q9BY67	Q9by67 homo sapien
126	134	6.4	1946	2	Q68J72	Q68j72 apis mellif
127	134	6.4	2217	2	Q8AV57	Q8av57 gallus gall
128	134	6.4	2623	2	Q6WR10	Q6wr10 homo sapien
129	133.5	6.4	321	2	Q68FQ2	Q68fq2 rattus norv
130	133.5	6.4	434	2	Q6DN72	Q6dn72 homo sapien
131	133.5	6.4	484	2	Q26475	Q26475 schistocerc
132	133.5	6.4	532	2	Q6NNU3	Q6nnu3 drosophila
133	133.5	6.4	532	2	Q9VLF0	Q9vlf0 drosophila
134	133.5	6.4	1164	2	Q66MN5	Q66mn5 drosophila
135	133.5	6.4	5175	2	Q810L3	Q810l3 caenorhabdi
136	133.5	6.4	5175	2	Q810L3	Q810l3 caenorhabdi
137	133.5	6.4	5198	2	Q76518	Q76518 caenorhabdi
138	133	6.3	285	2	Q8VE93	Q8ve93 mus musculu
139	133	6.3	349	1	LACH_SCHAM	Q26474 schistocerc
140	133	6.3	948	2	Q9VME2	Q9vme2 drosophila
141	133	6.3	1730	2	Q7YRQ7	Q7yrq7 sus scrofa
142	132.5	6.3	298	2	Q9J159	Q9j159 m vascular
143	132.5	6.3	641	2	Q86SD2	Q86sd2 ciona intes
144	132.5	6.3	765	2	Q9BKQ1	Q9bkq1 aplysia cal
145	132.5	6.3	765	2	Q9TW44	Q9twa4 aplysia cal
146	132.5	6.3	812	2	Q9BKQ0	Q9bkq0 aplysia cal
147	132.5	6.3	812	2	Q9TWA5	Q9twa5 aplysia cal
148	132.5	6.3	932	2	Q9BKp9	Q9bkp9 aplysia cal
149	132.5	6.3	932	2	Q9TWA6	Q9twa6 aplysia cal
150	132.5	6.3	1065	1	LIG2_HUMAN	Q94898 homo sapien
151	132.5	6.3	1369	1	NFAS_CHICK	Q42414 gallus gall
152	132	6.3	296	2	Q640C0	Q640c0 xenopus lae
153	132	6.3	300	2	Q78YQ7	Q78yq7 xenopus lae
154	132	6.3	394	2	Q6AYD4	Q6ayd4 rattus norv
155	132	6.3	464	2	Q6GL25	Q6gl25 xenopus tro
156	132	6.3	1746	2	Q8WY19	Q8wy19 homo sapien
157	132	6.3	2012	1	DSCA_HUMAN	Q60469 homo sapien
158	131.5	6.3	433	2	Q9V644	Q9v644 drosophila
159	131.5	6.3	467	1	SIL7_HUMAN	Q9y286 homo sapien
160	131.5	6.3	1247	2	Q7Q0S6	Q7q0s6 anopheles g
161	131.5	6.3	2673	2	Q96SC3	Q96sc3 homo sapien
162	131	6.2	259	2	Q9Y5B2	Q9y5b2 homo sapien
163	131	6.2	285	2	Q8BTK0	Q8btk0 mus musculu
164	131	6.2	309	2	Q91YV7	Q91yv7 mus musculu
165	131	6.2	1073	2	Q9W1T8	Q9w1t8 drosophila
166	131	6.2	1173	2	Q6NR54	Q6nr54 drosophila
167	131	6.2	4391	1	PGBM_HUMAN	P98160 homo sapien
168	130.5	6.2	272	2	Q7O356	Q7o356 mus musculu
169	130.5	6.2	456	2	Q8R5M8	Q8r5m8 mus musculu
170	130.5	6.2	702	2	Q69ZY8	Q69zy8 mus musculu
171	130	6.2	253	2	Q9DBH2	Q9dbh2 m mus muscu
172	130	6.2	316	2	Q8VE98	Q8ve98 mus musculu
173	130	6.2	445	2	Q8K3T6	Q8k3t6 mus musculu
174	130	6.2	515	1	PVRI_PIG	Q9gl76 sus scrofa
175	130	6.2	540	2	Q8N0Z9	Q8n0z9 homo sapien
176	130	6.2	582	2	Q8R4B5	Q8r4b5 mus musculu
177	130	6.2	915	2	Q8R4B3	Q8r4b3 mus musculu
178	130	6.2	955	1	MDG1_HUMAN	Q8nfp4 homo sapien
179	129.5	6.2	300	2	Q68SP0	Q68sp0 mus musculu
180	129.5	6.2	1040	1	AXO1_RAT	P22063 rattus norv
181	129.5	6.2	3375	1	UN52_CABEL	Q06561 caenorhabdi
182	129.5	6.2	6658	2	Q76281	Q76281 drosophila
183	129.5	6.2	8647	2	Q7KQP5	Q7kqp5 drosophila
184	129.5	6.2	8648	2	Q7KQP6	Q7kqp6 drosophila
185	129.5	6.2	8930	2	Q7KQP7	Q7kqp7 drosophila
186	129.5	6.2	8943	2	Q9V4F7	Q9v4f7 drosophila
187	129	6.1	208	2	Q80WN3	Q80wn3 mus musculu
188	129	6.1	295	2	Q9QYL6	Q9qyl6 mus musculu
189	129	6.1	295	2	Q9Z2H8	Q9z2h8 mus musculu
190	129	6.1	309	1	CD86_MOUSE	P42082 mus musculu
191	129	6.1	314	2	Q61238	Q61238 mus musculu
192	129	6.1	324	2	Q7TMH2	Q7tmh2 mus musculu
193	129	6.1	343	2	Q8R4Y0	Q8r4y0 mus musculu
194	129	6.1	356	2	Q64381	Q64381 mus musculu
195	129	6.1	445	2	Q8R4L1	Q8r4l1 mus musculu
196	129	6.1	1427	2	Q91562	Q91562 xenopus lae
197	129	6.1	1906	1	KMLS_CHICK	Q8r411 mus musculu
198	128.5	6.1	306	2	Q9QYL4	Q9qyl4 xenopus lae
199	128.5	6.1	775	2	Q6PF50	Q6pf50 xenopus lae
200	128.5	6.1	1040	1	AXO1_MOUSE	Q6i330 mus musculu
201	128.5	6.1	1386	2	Q8T172	Q8ti72 methanosarc
202	128.5	6.1	2053	2	Q81ZY4	Q81zy4 homo sapien
203	128	6.1	255	2	Q9VQ64	Q9vq64 drosophila
204	128	6.1	257	2	Q8R202	Q8r202 mus musculu
205	128	6.1	261	2	Q9D7L8	Q9d7l8 m mus muscu
206	128	6.1	343	2	Q8BY54	Q8by54 mus musculu
207	128	6.1	386	2	Q8BINO	Q8bin0 mus musculu
208	128	6.1	392	2	Q7PSN2	Q7psn2 anopheles g
209	128	6.1	977	2	Q96RD9	Q96rd9 homo sapien
210	128	6.1	2133	2	Q7PQG9	Q7pqg9 anopheles g
211	127.5	6.1	299	2	Q7Q8F3	Q7q8f3 anopheles g
212	127.5	6.1	442	2	Q6NW88	Q6nw88 brachydanio
213	127.5	6.1	1028	2	Q6INB5	Q6inb5 xenopus lae
214	127.5	6.1	1340	2	Q8ND42	Q8nda2 homo sapien
215	127.5	6.1	1496	2	Q92626	Q92626 homo sapien
216	127	6.1	282	2	Q8VIMI	Q8vimi mus musculu
217	127	6.1	282	2	Q7TPU2	Q7tpu2 mus musculu
218	127	6.1	337	1	OPCM_CHICK	Q98892 gallus gall
219	127	6.1	344	2	Q9DF61	Q9df61 gallus gall
220	127	6.1	725	1	NCA1_MOUSE	P13594 mus musculu
221	127	6.1	1115	2	Q90Z04	P13595 mus musculu
222	127	6.1	1249	2	Q7PPH8	Q7pph8 anopheles g
223	127	6.1	1555	2	Q7PPH8	Q7pph8 anopheles g
224	127	6.1	2053	2	Q8WXU7	Q8wxu7 homo sapien
225	127	6.1	2092	2	Q76MU9	Q76mu9 homo sapien
226	127	6.1	2113	2	Q8TDM9	Q8tdm9 homo sapien
227	126.5	6.0	318	2	Q91664	Q91664 xenopus lae
228	126.5	6.0	433	2	Q6DUJ83	Q6dj83 xenopus tro
229	126.5	6.0	499	1	SIL8_HUMAN	Q9nyz4 homo sapien
230	126.5	6.0	597	1	SIL8_HUMAN	Q951h0 pan troglod
231	126.5	6.0	812	2	Q8N6I2	Q8n6i2 homo sapien
232	126.5	6.0	865	2	Q68DA2	Q68da2 homo sapien
233	126.5	6.0	924	1	ICAS_HUMAN	Q9umf0 homo sapien
234	126.5	6.0	924	2	Q8TAM9	Q8tam9 homo sapien
235	126.5	6.0	986	2	Q6DG17	Q6dgl7 brachydanio
236	126.5	6.0	1056	2	Q90Z03	Q90z03 xenopus lae
237	126	6.0	378	2	Q66MN4	Q66mn4 petromyzon
238	126	6.0	413	2	Q7OBV2	Q7qbv2 anopheles g
239	126	6.0	463	2	SIL9_HUMAN	Q9y336 homo sapien
240	126	6.0	885	2	Q8HYV1	Q8hyv1 sus scrofa
241	126	6.0	886	2	Q8HYV2	Q8hyv2 sus scrofa
242	126	6.0	947	1	MUSK_CHICK	Q8axy6 gallus gall
243	126	6.0	1476	2	Q7QJ29	Q7qj29 anopheles g
244	125.5	6.0	303	2	Q7Q154	Q7q154 anopheles g
245	125.5	6.0	336	2	Q46551	Q46551 hylobates s
246	125.5	6.0	412	2	Q9R1E1	Q9r1e1 rattus norv
247	125.5	6.0	476	2	Q6AYP5	Q6ayp5 rattus norv
248	125.5	6.0	499	2	Q7Z728	Q7z728 homo sapien
249	125.5	6.0	626	2	Q6DCH3	Q6dch3 xenopus lae
250	125.5	6.0	707	2	Q7PWJ1	Q7pwj1 anopheles g

251	125.5	6.0	1443	2	Q8MTB2	Q8mtb2 drosophila	324	121.5	5.8	320	2	Q7Q0P8	Q7q0p8 anopheles g
252	125.5	6.0	1765	2	Q9VS30	Q9vs30 drosophila	325	121.5	5.8	337	2	P97268	P97268 cavia porce
253	125.5	6.0	1770	2	Q9VS29	Q9vs29 drosophila	326	121.5	5.8	344	1	CEA6_HUMAN	P40199 homo sapien
254	125	6.0	311	2	Q6DN73	Q6dn73 homo sapien	327	121.5	5.8	508	2	Q8CED8	Q8ced8 mus musculu
255	125	6.0	313	2	O57596	O57596 gallus gall	328	121.5	5.8	508	2	Q8R007	Q8r007 mus musculu
256	125	6.0	315	2	O9DG15	O9dg15 gallus gall	329	121.5	5.8	549	2	O9NQS3	O9nqs3 homo sapien
257	125	6.0	439	2	Q6GTU4	Q6gtu4 homo sapien	330	121.5	5.8	595	2	Q6ZRS5	Q6zrs5 homo sapien
258	125	6.0	467	2	Q91VT9	Q91vt9 mus musculu	331	121.5	5.8	1154	2	Q9QVN3	Q9qvn3 rattus sp.
259	125	6.0	510	2	Q96NY8	Q96ny8 homo sapien	332	121.5	5.8	1180	2	Q8T157	Q8t157 methanosarc
260	125	6.0	538	2	Q9NMQ7	Q9nmq7 homo sapien	333	121.5	5.8	1194	2	Q6PW35	Q6pw35 rattus norv
261	125	6.0	1006	2	Q6IDE9	Q6ide9 drosophila	334	121.5	5.8	1197	2	Q6PW38	Q6pw38 rattus norv
262	125	6.0	18412	2	Q7ZZ61	Q7zz61 brachydantio	335	121.5	5.8	1198	2	Q6PW37	Q6pw37 rattus norv
263	124.5	5.9	259	2	Q7ZZQ1	Q7zzq1 homo sapien	336	121.5	5.8	1206	2	Q6PW36	Q6pw36 rattus norv
264	124.5	5.9	344	2	O93242	O93242 gallus gall	337	121.5	5.8	1209	2	Q6PW39	Q6pw39 rattus norv
265	124.5	5.9	353	1	CEPU_CHICK	O90773 gallus gall	338	121.5	5.8	1214	1	NRCA_RAT	Q6pw36 rattus norv
266	124.5	5.9	387	2	Q86XK7	Q86xk7 homo sapien	339	121.5	5.8	1224	2	O00533	O00533 homo sapien
267	124.5	5.9	412	2	Q6MZS4	Q6mzs4 homo sapien	340	121.5	5.8	1299	2	Q6PW23	Q6pw23 rattus norv
268	124.5	5.9	815	2	Q805B9	Q805b9 brachydantio	341	121	5.8	366	2	Q6NVZ3	Q6nvz3 homo sapien
269	124.5	5.9	848	1	NCA1_HUMAN	P13591 homo sapien	342	121	5.8	390	2	Q66KX2	Q66kx2 xenopus lae
270	124.5	5.9	877	2	Q9GSH3	Q9gsh3 halocynthia	343	121	5.8	410	2	Q7YZA7	Q7yza7 bombyx mori
271	124	5.9	394	2	Q6DC16	Q6dc16 xenopus lae	344	121	5.8	528	2	P91670	P91670 drosophila
272	124	5.9	623	2	Q8BY18	Q8by18 mus musculu	345	121	5.8	538	2	Q28939	Q28939 sus scrofa
273	124	5.9	688	2	Q80ZE3	Q80ze3 mus musculu	346	121	5.8	858	2	O18466	O18466 hirudo medl
274	124	5.9	697	2	Q7PMJ7	Q7pmj7 anopheles g	347	121	5.8	1031	2	Q90YM2	Q90ym2 brachydantio
275	124	5.9	853	1	NCA1_BOVIN	P31836 bos taurus	348	121	5.8	1086	2	Q7QH02	Q7qh02 anopheles g
276	124	5.9	1011	2	Q24273	Q24273 drosophila	349	121	5.8	1155	2	Q7Q3K8	Q7q3k8 anopheles g
277	124	5.9	1240	1	NFAS_HUMAN	O94856 homo sapien	350	121	5.8	1304	1	NRCA_HUMAN	Q92823 homo sapien
278	124	5.9	1240	1	NFAS_MOUSE	O810u3 mus musculu	351	120.5	5.7	163	2	Q8K1H8	Q8k1h8 mus musculu
279	124	5.9	1240	1	NFAS_RAT	P97685 rattus norv	352	120.5	5.7	202	2	Q6NTA1	Q6nta1 homo sapien
280	124	5.9	1251	2	Q6ZQ54	Q6zq54 mus musculu	353	120.5	5.7	265	2	Q7PTU3	Q7puu3 anopheles g
281	124	5.9	1366	1	ROB3_MOUSE	Q9z214 mus musculu	354	120.5	5.7	358	2	Q9Q490	O43699 brachydantio
282	123.5	5.9	336	1	C226_HUMAN	Q15762 homo sapien	355	120.5	5.7	442	1	SLI6_HUMAN	Q43699 homo sapien
283	123.5	5.9	338	1	LAMP_CHICK	O98919 gallus gall	356	120.5	5.7	449	2	Q9UE16	Q9ue16 homo sapien
284	123.5	5.9	350	2	O02869	O02869 gallus gall	357	120.5	5.7	529	2	Q91V87	Q91v87 mus musculu
285	123.5	5.9	383	2	Q75ML9	Q75ml9 homo sapien	358	120.5	5.7	549	2	Q9JLB9	Q9jlb9 mus musculu
286	123.5	5.9	412	2	Q63611	Q63611 rattus norv	359	120.5	5.7	1940	2	Q6PDN3	Q6pdn3 mus musculu
287	123.5	5.9	454	2	Q91W54	Q91w54 mus musculu	360	120	5.7	312	2	Q6UXG6	Q6uxg6 homo sapien
288	123.5	5.9	521	1	CEA1_MOUSE	P31809 mus musculu	361	120	5.7	316	2	Q9BXR1	Q9bxr1 homo sapien
289	123.5	5.9	521	2	Q925P3	Q925p3 mus musculu	362	120	5.7	333	1	AMAL_DROME	P15364 drosophila
290	123.5	5.9	538	2	Q29123	Q29123 sus scrofa	363	120	5.7	341	2	Q7K5X2	Q7k5x2 drosophila
291	123.5	5.9	595	1	SILL_HUMAN	Q96pq1 homo sapien	364	120	5.7	410	2	Q6R3L9	Q6r3l9 bombyx mand
292	123.5	5.9	605	2	Q921P2	O921p2 mus musculu	365	120	5.7	483	2	Q9DBB8	Q9dbb8 mus musculu
293	123.5	5.9	800	2	Q918X3	O918x3 brachydantio	366	120	5.7	510	2	Q96K15	Q96k15 homo sapien
294	123.5	5.9	838	2	Q8BQ96	Q8bq96 mus musculu	367	120	5.7	662	2	O8MJZ6	Q8mjz6 par troglod
295	123.5	5.9	838	2	Q8C4B2	Q8c4b2 mus musculu	368	120	5.7	1093	1	LIG1_HUMAN	Q96ja1 homo sapien
296	123.5	5.9	875	2	Q91ZY7	Q91zy7 mus musculu	369	119.5	5.7	298	1	JMAM2_HUMAN	P57087 homo sapien
297	123.5	5.9	1091	1	NCA1_CHICK	P13590 gallus gall	370	119.5	5.7	298	2	Q6YNC1	Q6ync1 homo sapien
298	123.5	5.9	1151	2	Q9QVN5	Q9qvn5 rattus sp.	371	119.5	5.7	450	2	Q9VR25	Q9vr25 drosophila
299	123.5	5.9	1256	1	NRCA_MOUSE	O810u4 mus musculu	372	119.5	5.7	520	2	Q925P2	Q925p2 mus musculu
300	123.5	5.9	1723	2	Q8CHB2	Q8chb2 mus musculu	373	119.5	5.7	529	2	Q7TQM3	Q7tqm3 rattus norv
301	123.5	5.9	1842	2	Q81ZY3	O81zy3 homo sapien	374	119.5	5.7	547	1	CD19_MOUSE	P25918 mus musculu
302	123	5.9	265	2	Q9NGZ0	Q9ngz0 spodoptera	375	119.5	5.7	672	2	Q9PD06	Q9pd06 mus musculu
303	123	5.9	304	2	Q9BPN5	Q9bpn5 caenorhabdt	376	119.5	5.7	725	2	Q73634	Q73634 drosophila
304	123	5.9	344	1	NTRI_HUMAN	O9p121 homo sapien	377	119.5	5.7	858	2	Q66X47	Q66x47 xenopus lae
305	123	5.9	373	2	Q7KYP5	Q7kyp5 homo sapien	378	119.5	5.7	917	1	ICAS_MOUSE	Q66x25 mus musculu
306	123	5.9	464	2	Q16170	Q16170 homo sapien	379	119.5	5.7	1643	2	Q7QGT8	Q7qgt8 anopheles g
307	123	5.9	467	2	Q8C6F2	Q8c6f2 mus musculu	380	119.5	5.7	1950	2	Q80YN8	Q80yn8 mus musculu
308	123	5.9	468	2	Q96CA7	Q96ca7 homo sapien	381	119.5	5.7	334	2	O02870	O02870 gallus gall
309	123	5.9	526	1	CEA1_HUMAN	P13688 homo sapien	382	119	5.7	391	2	Q7QJG1	Q7qjg1 anopheles g
310	123	5.9	779	2	Q97136	O97136 manduca sex	383	119	5.7	410	2	Q6R3M0	Q6r3mo bombyx mori
311	123	5.9	837	2	O97137	Q97137 manduca sex	384	119	5.7	727	2	Q6RK32	Q6rk32 rattus norv
312	123	5.9	1694	1	SN_MOUSE	Q62230 mus musculu	385	119	5.7	769	2	Q8NT15	Q8nt15 homo sapien
313	122.5	5.8	400	2	Q8HY16	Q8hy16 cebus apeli	386	119	5.7	806	1	FGR3_HUMAN	P22607 homo sapien
314	122.5	5.8	738	1	PECL_HUMAN	P16284 homo sapien	387	119	5.7	837	2	Q6RKX3	Q6rkb3 rattus norv
315	122.5	5.8	761	1	NCA2_HUMAN	P13592 homo sapien	388	119	5.7	907	2	Q9NEG0	Q9neg0 drosophila
316	122.5	5.8	1032	2	Q8UVD6	Q8uvd6 brachydantio	389	119	5.7	1091	1	LIG1_MOUSE	P70193 mus musculu
317	122.5	5.8	1284	1	NRCA_CHICK	P35331 gallus gall	390	119	5.7	1994	2	Q6ZPB2	Q6zpb2 mus musculu
318	122.5	5.8	1419	2	Q98SW3	Q98sw3 brachydantio	391	119	5.7	2176	2	Q6V4S5	Q6v4s5 mus musculu
319	122	5.8	240	2	Q6MG96	Q6mg96 rattus norv	392	119	5.7	4179	2	Q9W4Y4	Q9w4y4 drosophila
320	122	5.8	410	2	Q6R3M2	Q6r3m2 bombyx mori	393	119	5.7	4463	2	Q8MLD8	Q8mld8 drosophila
321	122	5.8	1036	1	AXO1_CHICK	P28685 gallus gall	394	119	5.7	9270	2	Q8MLD9	Q8mld9 drosophila
322	122	5.8	1166	2	Q9QVN4	Q9qvn4 rattus sp.	395	119	5.7	26926	2	Q10466	Q10466 homo sapien
323	121.5	5.8	244	2	Q95T89	Q95t89 drosophila	396	119	5.7				

397	119	5.7	26926	2	Q8WZB3	Q8wzb3 homo sapien
398	118.5	5.6	152	2	Q8BSQ8	Q8bsq8 mus musculu
399	118.5	5.6	262	2	Q6UXZ0	Q6uxz0 homo sapien
400	118.5	5.6	413	2	Q7QBV1	Q7qbv1 anopheles g
401	118.5	5.6	458	2	Q63093	Q63093 rattus norv
402	118.5	5.6	462	2	Q7RTW1	Q7rtw1 homo sapien
403	118.5	5.6	519	1	ECTO_RAT	P16573 rattus norv
404	118.5	5.6	640	2	Q7RTV8	Q7rtv8 homo sapien
405	118.5	5.6	1561	2	Q924D2	Q924d2 mus musculu
406	118	5.6	163	2	Q9NVJ5	Q9nvj5 homo sapien
407	118	5.6	289	2	Q9QYL5	Q9qyl5 mus musculu
408	118	5.6	344	1	NTRI_MOUSE	Q99pj0 mus musculu
409	118	5.6	344	2	Q8BG33	Q8bg33 m mus muscu
410	118	5.6	359	2	Q7ZX17	Q7zx17 xenopus lae
411	118	5.6	413	2	Q9VAR6	Q9var6 drosophila
412	118	5.6	501	2	Q6Q147	Q6q147 bos taurus
413	118	5.6	547	1	ICA3_HUMAN	P32942 homo sapien
414	118	5.6	547	2	Q6PD68	Q6pd68 homo sapien
415	118	5.6	782	2	Q61563	Q61563 mus musculu
416	118	5.6	782	2	Q9ESAS	Q9esas rattus norv
417	118	5.6	807	2	Q6NY23	Q6ny23 brachydanio
418	118	5.6	837	1	NCM2_MOUSE	Q35136 mus musculu
419	118	5.6	1103	2	Q6ONF3	Q6gnf3 canis faml
420	118	5.6	1338	1	VGRI_HUMAN	P17948 h vascular
421	118	5.6	4824	2	Q95YML	Q95ym1 procambarus
422	118	5.6	17352	2	Q95YML	Q95ym2 procambarus
423	117.5	5.6	338	1	LAMP_HUMAN	Q13449 homo sapien
424	117.5	5.6	340	2	Q9W3N2	Q9w3n2 drosophila
425	117.5	5.6	344	2	Q13774	Q13774 homo sapien
426	117.5	5.6	509	2	Q920C2	Q920c2 mus musculu
427	117.5	5.6	533	2	Q8NCB6	Q8ncb6 homo sapien
428	117.5	5.6	1028	2	P97528	P97528 rattus norv
429	117.5	5.6	1056	2	Q7ZW34	Q7zw34 brachydanio
430	117.5	5.6	1092	1	NCA2_XENLA	P36335 xenopus lae
431	117.5	5.6	1302	1	NRG_DROME	P20241 drosophila
432	117.5	5.6	1389	2	Q9OZ69	Q9oz69 brachydanio
433	117.5	5.6	2008	2	Q9VEJ5	Q9vej5 drosophila
434	117.5	5.6	2046	2	Q7KSE9	Q7kse9 drosophila
435	117.5	5.6	8625	2	Q86GD6	Q8egd6 procambarus
436	117.5	5.6	351	2	Q6WEB2	Q6web2 brachisto
437	117	5.6	401	2	Q7PSS8	Q7ps88 anopheles g
438	117	5.6	448	2	Q9JHL7	Q9jhl7 rattus norv
439	117	5.6	459	2	Q9JHL6	Q9jhl6 rattus norv
440	117	5.6	484	2	Q6BEO0	Q6be00 xenopus lae
441	117	5.6	650	1	LIB1_HUMAN	Q8nh16 h leukocyte
442	117	5.6	739	1	VCA1_RAT	P29534 rattus norv
443	117	5.6	858	1	NCAL_RAT	P13596 rattus norv
444	117	5.6	1062	2	Q8BKG3	Q8bk93 mus musculu
445	117	5.6	1445	2	Q63155	Q63155 rattus norv
446	117	5.6	1447	1	DCC_HUMAN	P43146 homo sapien
447	117	5.6	2164	2	Q9IAR9	Q9iar9 gallus gall
448	116.5	5.6	285	2	Q7PNI4	Q7pni4 anopheles g
449	116.5	5.6	316	2	Q8WPB3	Q8wpb3 drosophila
450	116.5	5.6	338	1	LAMP_RAT	Q62813 rattus norv
451	116.5	5.6	341	1	LAMP_MOUSE	Q8b1k3 mus musculu
452	116.5	5.6	421	2	Q7PV30	Q7pv30 anopheles g
453	116.5	5.6	474	2	Q7PKX3	Q7pkx3 anopheles g
454	116.5	5.6	554	2	Q9W4R3	Q9w4r3 drosophila
455	116.5	5.6	620	2	Q6IGL3	Q6igl3 drosophila
456	116.5	5.6	806	1	CEK2_CHICK	P18460 gallus gall
457	116.5	5.6	899	2	Q7PQM9	Q7pqm9 anopheles g
458	116.5	5.6	972	2	Q26614	Q26614 strongyloce
459	116.5	5.6	1040	1	AXO1_HUMAN	Q02246 homo sapien
460	116.5	5.6	1051	1	PTK7_CHICK	Q91048 gallus gall
461	116.5	5.6	1598	2	Q9P214	Q9p214 homo sapien
462	116	5.5	237	2	Q6DQX5	Q6dqx5 oryctolagus
463	116	5.5	316	2	Q6UX12	Q6ux12 homo sapien
464	116	5.5	333	1	C226_MOUSE	Q8k4f0 mus musculu
465	116	5.5	344	1	NTRI_RAT	Q62718 rattus norv
466	116	5.5	344	2	Q6B014	Q6b014 homo sapien
467	116	5.5	435	2	Q8N3J6	Q8n3j6 homo sapien
468	116	5.5	1027	2	Q90W79	Q90w79 gallus gall
469	116	5.5	1189	2	Q9P2J2	Q9p2j2 homo sapien
470	116	5.5	1447	1	DCC_MOUSE	P70211 mus musculu
471	116	5.5	1709	1	SN_HUMAN	Q9bz22 homo sapien
472	115.5	5.5	390	2	Q6P500	Q6p500 rattus norv
473	115.5	5.5	421	2	Q7QLK4	Q7qlk4 anopheles g
474	115.5	5.5	437	2	Q812P8	Q81zpx8 homo sapien
475	115.5	5.5	485	1	PODX_RAT	Q9wtq2 rattus norv
476	115.5	5.5	527	2	Q9ERF7	Q9erf7 cricetus
477	115.5	5.5	590	2	Q6PAT5	Q6pat5 mus musculu
478	115.5	5.5	725	2	Q73633	Q73633 xenopus lae
479	115.5	5.5	731	2	Q8SPI6	Q8spi6 macropus eu
480	115.5	5.5	828	2	Q9DGK3	Q9dgk3 xenopus lae
481	115.5	5.5	1252	2	Q96DN3	Q96dn3 homo sapien
482	115.5	5.5	1255	2	Q7Z3Z9	Q7z3z9 homo sapien
483	115.5	5.5	1255	2	Q7YQL8	Q7yql8 pan troglod
484	115.5	5.5	1257	1	CAML_HUMAN	P32004 homo sapien
485	115.5	5.5	1493	1	NEO1_MOUSE	P97798 mus musculu
486	115.5	5.5	4001	2	Q9N2F7	Q9n2p7 drosophila
487	115.5	5.5	4796	2	Q9NL88	Q9nl88 drosophila
488	115.5	5.5	4796	2	Q9W055	Q9w055 drosophila
489	115.5	5.5	16215	2	Q9NFS3	Q9nfs3 drosophila
490	115.5	5.5	17903	2	Q7RTL4	Q7rtl4 drosophila
491	115.5	5.5	18074	2	Q917U4	Q9i7u4 drosophila
492	115	5.5	217	2	Q6KGN0	Q6kgn0 bacterioph
493	115	5.5	237	2	Q8CG82	Q8cg82 mus musculu
494	115	5.5	294	2	Q6KGN1	Q6kgn1 bacterioph
495	115	5.5	399	2	Q8N772	Q8n772 homo sapien
496	115	5.5	424	2	Q8C6W0	Q8c6w0 mus musculu
497	115	5.5	510	2	Q9JLB8	Q9jlb8 mus musculu
498	115	5.5	602	2	Q86YJ9	Q86yj9 homo sapien
499	115	5.5	650	2	Q8NA84	Q8na84 homo sapien
500	115	5.5	837	2	Q7Z7F2	Q7z7f2 homo sapien
501	115	5.5	1109	2	Q6P5H3	Q6p5h3 mus musculu
502	115	5.5	1125	2	Q7QEC1	Q7qec1 anopheles g
503	115	5.5	1209	2	P70232	P70232 mus musculu
504	115	5.5	1302	1	VGRI_BRARE	Q8abx3 brachydanio
505	115	5.5	2403	2	Q8MLD5	Q8mld5 drosophila
506	115	5.5	7210	2	Q9V7G8	Q9v7g8 drosophila
507	114.5	5.5	336	1	C226_MACMU	O18906 macaca mula
508	114.5	5.5	345	2	Q6GM08	Q6gm08 xenopus lae
509	114.5	5.5	363	2	Q6NV41	Q6nv41 brachydanio
510	114.5	5.5	412	2	Q8HY14	Q8hy14 oryctolagus
511	114.5	5.5	458	2	Q61351	Q61351 mus musculu
512	114.5	5.5	489	2	Q7PGL7	Q7pgl7 anopheles g
513	114.5	5.5	497	2	Q9BXN7	Q9bxn7 homo sapien
514	114.5	5.5	504	2	Q8N441	Q8n441 homo sapien
515	114.5	5.5	504	2	Q9H4D7	Q9h4d7 homo sapien
516	114.5	5.5	517	1	PVR1_HUMAN	Q15223 homo sapien
517	114.5	5.5	521	2	Q61352	Q61352 mus musculu
518	114.5	5.5	525	2	Q7PZS8	Q7pzs8 anopheles g
519	114.5	5.5	530	1	PVR2_MOUSE	P32507 mus musculu
520	114.5	5.5	530	2	Q80XJ5	Q80xj5 mus musculu
521	114.5	5.5	538	1	PVR2_HUMAN	Q92692 homo sapien
522	114.5	5.5	551	2	Q8MSN7	Q8msn7 drosophila
523	114.5	5.5	719	2	Q66IV0	Q66iv0 xenopus lae
524	114.5	5.5	956	2	Q9W4T9	Q9w4t9 drosophila
525	114.5	5.5	959	2	Q9N9Y9	Q9n9y9 drosophila
526	114.5	5.5	975	2	Q97174	Q97174 drosophila
527	114.5	5.5	1088	1	NCAL_XENLA	P16170 xenopus lae
528	114.5	5.5	1415	2	Q94155	Q94155 caenorhabdi
529	114.5	5.5	5604	2	Q8WZ53	Q8wz53 homo sapien
530	114	5.4	235	2	Q75296	Q75296 homo sapien
531	114	5.4	323	2	Q9BDM2	Q9bdm2 cercopithec
532	114	5.4	337	2	Q6DFY2	Q6dfy2 mus musculu
533	114	5.4	401	2	Q08835	Q08835 cercopithec
534	114	5.4	403	2	Q8HY15	Q8hy15 lemur cat
535	114	5.4	438	2	Q9JLB7	Q9jlb7 mus musculu
536	114	5.4	544	1	ICA3_BOVIN	Q28125 bos taurus
537	114	5.4	545	2	Q9VCT4	Q9vct4 drosophila
538	114	5.4	602	1	NRG1_CHICK	Q05199 gallus gall
539	114	5.4	645	2	Q8MJZ5	Q8mjz5 pan troglod
540	114	5.4	773	1	P1832	P01832 oryctolagus
541	114	5.4	795	2	Q90YMO	Q90ymo brachydanio
542	114	5.4	1028	2	Q8C6X1	Q8c6x1 mus musculu

543	114	5.4	1028	2	Q9JMB8	Q9jmb8 mus musculu	616	111.5	5.3	816	2	Q8NFA5	Q8nfas homo sapien
544	114	5.4	1045	2	Q86T37	Q86t37 homo sapien	617	111.5	5.3	869	1	MUSK_HUMAN	O15146 homo sapien
545	114	5.4	1073	2	Q9TX18	Q9txi8 caenorhabdi	618	111.5	5.3	1060	2	Q9QZ13	O9qz13 rattus norv
546	114	5.4	1097	1	PGDR_RAT	Q05030 rattus norv	619	111.5	5.3	1070	2	Q6IQ54	Q6iq54 homo sapien
547	114	5.4	1177	2	Q6GQB1	Q6gqbl xenopus lae	620	111	5.3	252	2	Q8WWT6	Q8wvt6 homo sapien
548	114	5.4	1320	2	Q96KF5	Q96kf5 homo sapien	621	111	5.3	283	2	Q8K091	Q8k091 mus musculu
549	114	5.4	1320	2	Q86TC9	Q86tc9 homo sapien	622	111	5.3	395	2	Q8BXJ7	Q8bxj7 m mus muscu
550	114	5.4	1735	2	Q7Q9I6	Q7q9i6 anopheles g	623	111	5.3	395	2	Q8BZP4	Q8bzip4 mus musculu
551	113.5	5.4	232	2	Q7PJ18	Q7pj18 anopheles g	624	111	5.3	960	2	Q7PV74	Q7pv74 anopheles g
552	113.5	5.4	284	2	Q9NX42	Q9nx42 homo sapien	625	111	5.3	1026	2	Q8IWW2	Q8iww2 homo sapien
553	113.5	5.4	296	2	Q6PJ56	Q6pj56 homo sapien	626	111	5.3	1228	2	Q8MRA3	Q8mra3 drosophila
554	113.5	5.4	316	2	Q8WP94	Q8wp94 drosophila	627	111	5.3	1235	2	Q86BD5	Q86bd5 drosophila
555	113.5	5.4	327	2	Q96IQ7	Q96iq7 homo sapien	628	111	5.3	1235	2	Q86BD5	Q86bd5 drosophila
556	113.5	5.4	382	2	Q7PSH7	Q7psh7 anopheles g	629	111	5.3	1235	2	Q9V787	Q9v787 drosophila
557	113.5	5.4	388	2	Q8NC34	Q8nc34 homo sapien	630	111	5.3	8081	2	Q7Z120	O01761 caenorhabdi
558	113.5	5.4	417	1	PVR_CERAE	P32506 cercopithec	631	110.5	5.3	316	2	Q8WP58	Q8wp58 drosophila
559	113.5	5.4	534	2	Q8NB18	Q8nb18 homo sapien	632	110.5	5.3	370	2	Q6MZQ3	Q6mzq3 homo sapien
560	113.5	5.4	754	2	Q8BZ76	Q8bz76 m mus muscu	633	110.5	5.3	390	2	Q96AP7	Q96ap7 homo sapien
561	113.5	5.4	771	2	Q7QBY8	Q7qey8 anopheles g	634	110.5	5.3	390	2	Q96T50	Q96t50 homo sapien
562	113.5	5.4	939	2	Q967X6	Q967x6 drosophila	635	110.5	5.3	395	2	Q6IE78	Q6ie78 paratichthy
563	113.5	5.4	939	2	Q9VB35	Q9vb35 drosophila	636	110.5	5.3	404	2	Q8BYP1	Q8byp1 mus musculu
564	113.5	5.4	1248	2	Q9XT41	Q9xt41 cercopithec	637	110.5	5.3	422	2	Q96PJ3	Q96pj3 homo sapien
565	113.5	5.4	1255	2	Q7YQL7	Q7yql7 pongo pygma	638	110.5	5.3	500	2	Q6UX41	Q6ux41 homo sapien
566	113.5	5.4	1386	1	ROB3_HUMAN	Q96ms0 homo sapien	639	110.5	5.3	513	2	O00481	O00481 homo sapien
567	113.5	5.4	1614	2	Q8UYD7	Q8uyd7 xenopus lae	640	110.5	5.3	515	2	Q96PJ5	Q96pj5 homo sapien
568	113.5	5.4	1675	2	Q98SM4	Q98sw4 brachydanio	641	110.5	5.3	515	2	Q96RE0	Q96reo0 homo sapien
569	113	5.4	340	2	Q7Q807	Q7q807 anopheles g	642	110.5	5.3	544	2	Q6UXI8	Q6uxi8 homo sapien
570	113	5.4	430	2	Q8NAF1	Q8naf1 homo sapien	643	110.5	5.3	546	2	Q80X70	Q80x70 mus musculu
571	113	5.4	430	2	Q7QGS8	Q7qgs8 anopheles g	644	110.5	5.3	548	2	Q99NB3	Q99nb3 mus musculu
572	113	5.4	636	2	Q22040	Q22040 caenorhabdi	645	110.5	5.3	662	2	Q8MQZ9	Q8mqz9 drosophila
573	113	5.4	816	2	Q91285	Q91285 pleurodeles	646	110.5	5.3	662	2	Q8MQZ9	Q8mqz9 drosophila
574	113	5.4	1277	1	CAML_FUGRU	Q98902 fugu rubrip	647	110.5	5.3	789	1	KIR1_RAT	Q9vgd0 drosophila
575	113	5.4	3100	2	Q7KYN5	Q7kyn5 homo sapien	648	110.5	5.3	800	2	Q9JHX9	Q9jhx9 rattus norv
576	113	5.4	4650	2	Q15598	Q15598 homo sapien	649	110.5	5.3	1889	2	Q7Q0X2	Q7q0x2 anopheles g
577	112.5	5.4	226	2	Q7PYG1	Q7pyg1 anopheles g	650	110	5.2	218	2	Q6ZMC6	Q6zmc6 homo sapien
578	112.5	5.4	338	2	Q7Z3W6	Q7z3w6 homo sapien	651	110	5.2	428	2	Q96PJ6	Q96pj6 homo sapien
579	112.5	5.4	345	1	OPCM_HUMAN	Q14982 homo sapien	652	110	5.2	483	2	Q7SX76	Q7sx76 brachydanio
580	112.5	5.4	362	2	Q9JHQ1	Q9jhq1 rattus norv	653	110	5.2	626	1	MAG_RAT	P07722 rattus norv
581	112.5	5.4	363	2	O46147	O46147 onchocerca	654	110	5.2	637	2	Q7RTW3	Q7rtw3 homo sapien
582	112.5	5.4	437	2	Q8NPF6	Q8nfp6 homo sapien	655	110	5.2	741	2	Q6RCF4	Q6rcf4 vibrionphage
583	112.5	5.4	440	2	Q6ZMD4	Q6zmd4 homo sapien	656	110	5.2	815	2	Q8AYP3	Q8ayp3 brachydanio
584	112.5	5.4	639	1	NRG1_HUMAN	Q02297 h pro-neure	657	110	5.2	837	1	NCM2_HUMAN	O15394 homo sapien
585	112.5	5.4	743	2	Q6R6B2	Q6r6b2 vibrionphage	658	110	5.2	1378	1	ROB2_HUMAN	Q9hck4 homo sapien
586	112.5	5.4	1259	1	CAML_RAT	Q05695 rattus norv	659	110	5.2	1391	2	O8N3I4	O8n3i4 hitudo medi
587	112.5	5.4	1259	2	Q6PGJ3	Q6pgj3 mus musculu	660	110	5.2	1880	2	O18465	O18465 caenorhabdi
588	112.5	5.4	1342	2	Q9GPP6	Q9gpp6 drosophila	661	110	5.2	2389	2	Q6BEQ6	Q6beq6 caenorhabdi
589	112.5	5.4	1342	2	Q9VPE7	Q9vpz7 drosophila	662	109.5	5.2	307	2	O54947	O54947 cercocobus
590	112.5	5.4	2029	1	LAR_DROME	P16621 drosophila	663	109.5	5.2	323	2	Q9BDB8	Q9bdb8 caenorhabdi
591	112.5	5.4	2029	2	Q9VTS8	Q9vts8 drosophila	664	109.5	5.2	334	2	O8I9N0	Q8i9n0 brachiolesto
592	112.5	5.4	2224	2	Q9U1M1	Q9u1m1 drosophila	665	109.5	5.2	345	1	OPCM_HUMAN	P32736 rattus norv
593	112	5.3	352	1	NEGR_HUMAN	Q7z3b1 homo sapien	666	109.5	5.2	349	1	CEBA8_HUMAN	Q7qbc5 anopheles g
594	112	5.3	387	2	Q64JA4	Q64ja4 pan troglod	667	109.5	5.2	477	2	Q7QBC5	Q7qbc5 anopheles g
595	112	5.3	829	2	Q9PSV8	Q9psv8 xenopus lae	668	109.5	5.2	526	1	BUTY_HUMAN	Q6uxj4 homo sapien
596	112	5.3	913	2	Q8T3E5	Q8t3e5 caenorhabdi	669	109.5	5.2	548	2	Q9H458	Q9h458 homo sapien
597	112	5.3	928	2	Q19128	Q19128 caenorhabdi	670	109.5	5.2	526	2	Q9Z133	Q9z133 rattus norv
598	112	5.3	946	2	Q07153	Q07153 torpedo cal	671	109.5	5.2	595	2	Q90720	Q90720 gallus gall
599	112	5.3	955	2	Q8MQ86	Q8mq86 caenorhabdi	672	109.5	5.2	800	2	Q7TSI8	Q7tsi8 mus musculu
600	112	5.3	1066	2	Q8MSR5	Q8msr5 drosophila	673	109.5	5.2	801	1	FGR3_MOUSE	Q61851 mus musculu
601	112	5.3	1070	1	PTK7_HUMAN	Q13308 homo sapien	674	109.5	5.2	1336	1	VGR1_RAT	P53767 rattus norv
602	112	5.3	1212	2	Q95TG0	Q95tgo drosophila	675	109.5	5.2	1465	2	Q7TQGS	Q7tqgs mus musculu
603	112	5.3	1269	2	O01632	O01632 caenorhabdi	676	109.5	5.2	263	2	Q7TPW5	Q7tpw5 mus musculu
604	112	5.3	1273	2	O44928	O44928 caenorhabdi	677	109	5.2	283	2	Q7TPH5	Q7tpH5 mus musculu
605	112	5.3	1530	2	Q8Y479	Q8y479 listeria mo	678	109	5.2	283	2	Q7TSP5	Q7tsp5 mus musculu
606	112	5.3	3215	2	Q8IRV7	Q8irv7 drosophila	679	109	5.2	292	2	Q6UY47	Q6uy47 homo sapien
607	112	5.3	4117	2	Q8IRV9	Q8irv9 drosophila	680	109	5.2	328	2	O88775	O88775 rattus norv
608	112	5.3	4223	2	Q8MPN3	Q8mpn3 drosophila	681	109	5.2	345	2	P7PVU1	Q7pvu1 anopheles g
609	112	5.3	4228	2	Q8IRV8	Q8irv8 drosophila	682	109	5.2	417	2	PVR_HUMAN	P15151 homo sapien
610	112	5.3	7105	2	Q7PXW9	Q7pxw9 anopheles g	683	109	5.2	562	2	Q6YNR7	Q6ynr7 brachydanio
611	111.5	5.3	267	2	Q8NC05	Q8nc05 homo sapien	684	109	5.2	582	2	O80WN2	O80wn2 mus musculu
612	111.5	5.3	390	2	Q95KIT3	Q95ki3 macaca fasc	685	109	5.2	595	2	O68SN8	O68sn8 mus musculu
613	111.5	5.3	400	1	HPL4_MOUSE	Q80wm4 mus musculu	686	109	5.2	640	2	Q8BSM2	Q8bsm2 mus musculu
614	111.5	5.3	443	2	Q8N2F4	Q8n2f4 homo sapien	687	109	5.2	646	1	MU18_HUMAN	P43121 homo sapien
615	111.5	5.3	508	2	Q96LAS	Q96las homo sapien	688	109	5.2				

689	109	5.2	646	2	Q6PHR3	Q6phr3	homo sapien	762	107	5.1	442	2	Q6KAT6	Q6kat6	mus musculu
690	109	5.2	1106	2	Q8WX93	Q8wx93	homo sapien	763	107	5.1	515	1	PVR1_MOUSE	Q9jkt6	mus musculu
691	108.5	5.2	345	1	OPCM_BOVIN	P1834	bos taurus	764	107	5.1	515	2	Q6P9M9	Q6p9m9	mus musculu
692	108.5	5.2	348	1	NEGR_MOUSE	Q80z24	mus musculu	765	107	5.1	606	2	Q6ESS8	Q6es88	rattus norv
693	108.5	5.2	348	1	NEGR_RAT	Q9z0j8	rattus norv	766	107	5.1	622	2	Q9JKB2	Q9jkb2	mus musculu
694	108.5	5.2	416	2	Q7M048	Q7m048	rattus norv	767	107	5.1	648	2	Q9EPF2	Q9epf2	rattus norv
695	108.5	5.2	495	2	Q9HCY1	Q9hcy1	homo sapien	768	107	5.1	817	2	Q8JG38	Q8jg38	brachydanio
696	108.5	5.2	686	1	SILB_HUMAN	Q96rl6	homo sapien	769	107	5.1	879	1	FPRP_MOUSE	Q9wv91	mus musculu
697	108.5	5.2	705	2	Q8CBD3	Q8cbd3	mus musculu	770	107	5.1	2558	2	Q6NR91	Q6nr91	drosophila
698	108.5	5.2	757	1	KIR1_HUMAN	Q96j84	homo sapien	771	107	5.1	19066	2	Q801W8	Q801w8	brachydanio
699	108.5	5.2	807	2	Q6DD66	Q6dd66	xenopus lae	772	106.5	5.1	304	2	Q9CVA4	Q9cva4	mus musculu
700	108.5	5.2	818	2	Q9PSV9	Q9psv9	xenopus lae	773	106.5	5.1	354	1	HPL1_HORSE	Q28381	equus cabal
701	108.5	5.2	819	1	FGRI_CHICK	P21804	gallus gall	774	106.5	5.1	404	2	Q8BLQ9	Q8blq9	mus musculu
702	108.5	5.2	868	1	MUSK_MOUSE	Q61006	mus musculu	775	106.5	5.1	437	2	Q86YV1	Q86yv1	homo sapien
703	108.5	5.2	878	2	Q9GV22	Q9gv22	mytilus gal	776	106.5	5.1	662	2	Q60926	Q60926	homo sapien
704	108.5	5.2	898	2	Q69Z26	Q69z26	mus musculu	777	106.5	5.1	719	2	Q704G1	Q70246	drosophila
705	108.5	5.2	1021	2	P79757	P79757	gallus gall	778	106.5	5.1	793	2	Q70246	Q70246	mus musculu
706	108.5	5.2	1028	2	Q9UQ52	Q9uq52	homo sapien	779	106.5	5.1	813	2	Q8BQC3	Q8bqc3	mus musculu
707	108.5	5.2	1114	2	Q9BWX1	Q9bwx1	homo sapien	780	106.5	5.1	822	1	FGRI_HUMAN	P11362	homo sapien
708	108.5	5.2	1115	2	Q6UXJ5	Q6uxj5	homo sapien	781	106.5	5.1	1227	2	Q21038	Q21038	caenorhabdi
709	108.5	5.2	1328	2	Q21043	Q21043	caenorhabdi	782	106.5	5.1	1232	2	Q90284	Q90284	caenorhabdi
710	108.5	5.2	1426	2	Q82Z11	Q82z11	enterococcu	783	106.5	5.1	1474	2	Q8T4M0	Q8t4m0	drosophila
711	108.5	5.2	2000	2	Q97791	Q97791	oryctolagus	784	106.5	5.1	1509	2	Q81PG1	Q81pg1	drosophila
712	108.5	5.2	2169	2	Q8AV58	Q8av58	gallus gall	785	106.5	5.1	1509	2	Q95P10	Q95p10	drosophila
713	108.5	5.2	4203	2	Q965G2	Q965g2	caenorhabdi	786	106	5.1	317	2	Q95P10	Q8bex4	cowpox viru
714	108.5	5.2	4219	2	Q9NL87	Q9nl87	caenorhabdi	787	106	5.1	381	2	Q8BEK4	Q8r4b1	mus musculu
715	108.5	5.2	4369	2	Q8MXD7	Q8mxd7	caenorhabdi	788	106	5.1	796	2	Q91287	Q91287	pleurodeles
716	108.5	5.2	4447	2	Q8MXD8	Q8mxd8	caenorhabdi	789	106	5.1	919	1	UNC5_CAEEL	Q26261	caenorhabdi
717	108.5	5.2	4488	2	Q97YX2	Q9cjk2	caenorhabdi	790	106	5.1	1040	1	EG15_CAEEL	Q10656	caenorhabdi
718	108.5	5.2	4736	2	Q7Y799	Q7ytc99	mytilus gal	791	106	5.1	1051	2	Q69ZT7	Q7j168	caenorhabdi
719	108.5	5.2	173	2	Q9UKD5	Q9jkd5	rattus norv	792	106	5.1	1081	2	Q7UL68	Q69zct7	mus musculu
720	108	5.1	286	2	Q4E535	Q4e535	bos taurus	793	106	5.1	1096	2	Q8MQ14	Q8mq14	caenorhabdi
721	108	5.1	325	2	Q95791	Q95791	homo sapien	794	106	5.1	1099	2	Q7TMR8	Q7tmr8	mus musculu
722	108	5.1	325	2	Q8HW98	Q8hw98	mus musculu	795	106	5.1	1185	2	Q7PRK4	Q7prk4	anopheles g
723	108	5.1	329	2	Q8N225	Q8n225	homo sapien	796	106	5.1	1388	2	Q7PRK4	Q7qkx0	anopheles g
724	108	5.1	333	2	Q8I9N2	Q8i9n2	branchiosto	797	106	5.1	1409	2	Q8J127	Q8j127	brachydanio
725	108	5.1	376	2	Q90271	Q90z71	brachydanio	798	106	5.1	1409	2	Q801M2	Q801m2	brachydanio
726	108	5.1	407	2	Q9D2J4	Q9d2j4	mus musculu	799	106	5.1	1428	2	Q8AY67	Q8ay67	brachydanio
727	108	5.1	509	2	Q9EQY5	Q9eqy5	m mman-g pr	800	106	5.1	1914	1	KMLS_HUMAN	Q15746	homo sapien
728	108	5.1	526	1	BUTY_BOVIN	P18892	bos taurus	801	106	5.1	1914	2	Q7Z4J0	Q7z4j0	homo sapien
729	108	5.1	605	2	Q6GNI9	Q6gnl9	xenopus lae	802	106	5.1	2222	2	Q7QEG7	Q7qeg7	anopheles g
730	108	5.1	614	2	Q6DDQ7	Q6ddq7	xenopus lae	803	105.5	5.0	318	2	Q8AYZ8	Q8ayz8	variola vir
731	108	5.1	868	1	MUSK_RAT	Q62838	rattus norv	804	105.5	5.0	318	2	Q8BEI5	Q8be15	variola vir
732	108	5.1	879	1	FPRP_RAT	Q62786	rattus norv	805	105.5	5.0	328	2	Q9Z109	Q9z109	mus musculu
733	108	5.1	922	2	Q904I3	Q904i3	brachydanio	806	105.5	5.0	394	2	Q6UXG0	Q6uxg0	homo sapien
734	108	5.1	1098	1	PGDR_MOUSE	P05622	mus musculu	807	105.5	5.0	394	2	Q6TCK9	Q6tck9	oryctolagus
735	108	5.1	1099	2	P97527	P97527	rattus norv	808	105.5	5.0	408	2	Q8IMQ4	Q8ik094	m hypothei
736	108	5.1	1109	2	Q8CE91	Q8ce91	mus musculu	809	105.5	5.0	408	2	Q91WP1	Q91wp1	mus musculu
737	108	5.1	1110	2	Q8CE73	Q8ce73	mus musculu	810	105.5	5.0	408	2	Q8BVF6	Q8bvf6	mus musculu
738	108	5.1	1150	2	Q8BS24	Q8bs24	mus musculu	811	105.5	5.0	527	2	Q6ZTR2	Q6ztr2	homo sapien
739	108	5.1	1244	2	Q69YJ3	Q69yj3	homo sapien	812	105.5	5.0	601	2	Q96CJ3	Q96cj3	homo sapien
740	108	5.1	1612	1	ROBI_MOUSE	Q89026	mus musculu	813	105.5	5.0	729	2	Q63827	Q63827	rattus norv
741	108	5.1	2325	2	Q9N3X8	Q9n3x8	caenorhabdi	814	105.5	5.0	731	2	Q8CFK8	Q8cfk8	mus musculu
742	107.5	5.1	278	2	Q9QYL3	Q9qyl3	mus musculu	815	105.5	5.0	733	2	Q60830	Q60830	mus musculu
743	107.5	5.1	350	2	Q99420	Q99420	homo sapien	816	105.5	5.0	733	2	Q80T10	Q80t10	mus musculu
744	107.5	5.1	350	2	Q8I9N1	Q8i9n1	branchiosto	817	105.5	5.0	739	2	Q28260	Q28260	canis famil
745	107.5	5.1	366	2	Q8N759	Q8n759	homo sapien	818	105.5	5.0	789	2	Q7PME2	Q7pme2	anopheles g
746	107.5	5.1	402	1	HPL4_HUMAN	Q86uw8	homo sapien	819	105.5	5.0	820	2	Q8CIM9	Q8cim9	mus musculu
747	107.5	5.1	429	2	Q96LĀ6	Q96la6	homo sapien	820	105.5	5.0	822	1	FGRI_MOUSE	P16092	mus musculu
748	107.5	5.1	531	2	Q659F2	Q659f2	homo sapien	821	105.5	5.0	822	1	FGRI_RAT	Q04589	rattus norv
749	107.5	5.1	659	2	Q6ZNM1	Q6znm1	homo sapien	822	105.5	5.0	822	2	Q608I8	Q608i8	mus musculu
750	107.5	5.1	660	2	Q7Z681	Q7z681	homo sapien	823	105.5	5.0	987	2	Q8Y2M8	Q7yzm8	caenorhabdi
751	107.5	5.1	789	1	KIR1_MOUSE	Q80w68	mus musculu	824	105.5	5.0	1036	2	Q8SWM3	Q8sww3	drosophila
752	107.5	5.1	800	2	Q99052	Q99052	mus musculu	825	105.5	5.0	1102	2	Q923W7	Q923w7	mus musculu
753	107.5	5.1	818	2	Q91742	Q91742	xenopus lae	826	105.5	5.0	1256	2	Q7KTI7	Q7kt17	drosophila
754	107.5	5.1	828	2	Q91743	Q91743	xenopus lae	827	105.5	5.0	1256	2	Q35158	Q35158	rattus norv
755	107.5	5.1	846	2	Q57577	Q57577	cynops pyrr	828	105.5	5.0	1390	2	Q9VN14	Q9vn14	drosophila
756	107.5	5.1	1026	2	Q62845	Q62845	rattus norv	829	105.5	5.0	1461	2	Q8T9F6	Q8t9f6	drosophila
757	107.5	5.1	1100	2	Q57576	Q57576	cynops pyrr	830	105.5	5.0	1503	2	Q7XTI8	Q7kt18	drosophila
758	107.5	5.1	1225	2	Q6GP61	Q6gp61	xenopus lae	831	105.5	5.0	1509	2	Q9VLQ8	Q9vlq8	drosophila
759	107.5	5.1	1235	2	Q95428	Q95428	homo sapien	832	105	5.0	145	2	Q9MZE4	Q9mze4	macaca mula
760	107	5.1	199	2	Q8NDI0	Q8ndi0	homo sapien	833	105	5.0	232	2	Q8B274	Q8b274	mus musculu
761	107	5.1	332	2	Q6UXG3	Q6uxg3	homo sapien	834	105	5.0	408	2	Q9VT83	Q9vt83	drosophila

835	105	5.0	509	2	Q91YK7	Q91YK7 mus musculus	908	103.5	4.9	1145	2	Q9BKL8	Q9bkl8 aplysia cal
836	105	5.0	622	2	Q9ESS5	Q9ess5 mus musculus	909	103.5	4.9	1331	2	Q7Q623	Q7q623 anopheles g
837	105	5.0	622	2	Q9R069	Q9r069 mus musculus	910	103.5	4.9	1513	2	Q90Z70	Q90z70 brachydanio
838	105	5.0	626	1	MAG_MOUSE	P20917 mus musculus	911	103.5	4.9	1651	1	ROB1_HUMAN	Q9y6n7 homo sapien
839	105	5.0	645	2	Q7RTW4	Q7rtw4 homo sapien	912	103.5	4.9	6048	2	Q7JN65	Q7jn65 caenorhabd1
840	105	5.0	646	2	Q95812	Q95812 homo sapien	913	103.5	4.9	6839	2	Q23550	Q23550 caenorhabd1
841	105	5.0	650	2	Q99X86	Q99x86 mus musculus	914	103.5	4.9	7158	2	Q23551	Q23551 caenorhabd1
842	105	5.0	708	1	KIR2_HUMAN	Q6uw16 homo sapien	915	103	4.9	229	2	Q7PUC4	Q7puc4 anopheles g
843	105	5.0	739	2	Q865F2	Q865f2 oryctolagus	916	103	4.9	415	2	Q60977	Q60977 mus musculus
844	105	5.0	810	2	Q9PS96	Q9ps96 xenopus lae	917	103	4.9	498	2	Q8BRT6	Q8brt6 mus musculus
845	105	5.0	862	1	CD22_MOUSE	P35329 mus musculus	918	103	4.9	606	2	Q6IRH8	Q6irh8 rattus norv
846	105	5.0	940	2	Q8NFA7	Q8nfa7 homo sapien	919	103	4.9	763	2	Q95YM9	Q95ym9 halocynthia
847	105	5.0	998	2	Q977Y2	Q977y2 thermoplasma	920	103	4.9	771	1	PIGR_MOUSE	Q70570 mus musculus
848	105	5.0	4816	2	Q8T103	Q8t103 bombyx mori	921	103	4.9	873	1	FAS2_DROME	Q7tpd3 drosophila
849	104.5	5.0	265	2	O02280	O02280 caenorhabd1	922	103	4.9	1470	1	ROB2_MOUSE	Q24463 drosophila
850	104.5	5.0	360	2	Q8MRE6	Q8mre6 drosophila	923	103	4.9	1742	2	Q24463	Q66gv2 xenopus lae
851	104.5	5.0	377	2	Q80V04	Q80v04 mus musculus	924	102.5	4.9	224	2	Q66GV2	Q66gm1 rattus norv
852	104.5	5.0	426	2	Q64HXS	Q64hx5 oncorhynchus	925	102.5	4.9	308	2	Q6PNM1	Q8be16 varicella vir
853	104.5	5.0	428	2	Q6F3J3	Q6f3j3 mus musculus	926	102.5	4.9	318	2	Q8BEI6	Q9qng4 varicella min
854	104.5	5.0	454	2	Q68D85	Q68d85 homo sapien	927	102.5	4.9	318	2	Q9QNG4	Q9bdm4 macaca mula
855	104.5	5.0	523	2	Q8K2H7	Q8k2h7 mus musculus	928	102.5	4.9	323	2	Q9BDM4	P03994 rattus norv
856	104.5	5.0	536	2	Q8BJE2	Q8bje2 mus musculus	929	102.5	4.9	354	1	HP11_RAT	Q819k2 branchiosto
857	104.5	5.0	538	2	Q9QYQ7	Q9qyq7 mus musculus	930	102.5	4.9	356	2	Q819K2	Q7qch7 anopheles g
858	104.5	5.0	582	2	Q95N25	Q95n25 bos taurus	931	102.5	4.9	399	2	Q7QCH7	Q27418 manduca sex
859	104.5	5.0	640	2	Q8BGM8	Q8bgh8 m mus muscu	932	102.5	4.9	413	2	Q27418	Q9wru4 macaca mula
860	104.5	5.0	640	2	Q8C031	Q8c031 mus musculus	933	102.5	4.9	423	2	Q9WRU4	Q710n3 homo sapien
861	104.5	5.0	722	2	Q6GNB3	Q6gnb3 xenopus lae	934	102.5	4.9	636	2	Q7LON3	Q9hcj2 homo sapien
862	104.5	5.0	920	2	Q9P232	Q9p232 homo sapien	935	102.5	4.9	640	2	Q9HCJ2	Q9c015 homo sapien
863	104.5	5.0	931	2	Q6KAM5	Q6kam5 mus musculus	936	102.5	4.9	992	2	Q9C0L5	Q28824 bos taurus
864	104.5	5.0	1026	2	Q94780	Q94780 homo sapien	937	102.5	4.9	1176	1	KMLS_BOVIN	Q81y15 homo sapien
865	104.5	5.0	1100	2	Q94779	Q94779 homo sapien	938	102.5	4.9	1184	2	O81Y15	O55005 rattus norv
866	104.5	5.0	1109	2	Q6AZB0	Q6azb0 mus musculus	939	102.5	4.9	1651	1	ROB1_RAT	Q6z895 homo sapien
867	104.5	5.0	1184	2	Q75339	Q75339 homo sapien	940	102	4.9	305	2	Q6ZS95	Q8bek8 vaccinia vi
868	104.5	5.0	1184	2	Q6UW99	Q6uw99 homo sapien	941	102	4.9	314	2	Q8BEK8	O00477 homo sapien
869	104.5	5.0	1377	1	NEO1_RAT	P97603 rattus norv	942	102	4.9	319	2	O00477	Q8ba95 homo sapien
870	104.5	5.0	1461	1	NEO1_HUMAN	Q92859 homo sapien	943	102	4.9	332	2	Q8TA95	Q9bu81 homo sapien
871	104.5	5.0	1503	2	Q8T4I8	Q8t4i8 drosophila	944	102	4.9	332	2	Q9BU81	Q76pa0 homo sapien
872	104.5	5.0	2222	2	Q97394	O97394 drosophila	945	102	4.9	334	2	Q76PA0	Q8ms24 drosophila
873	104.5	5.0	2230	2	Q86BQ7	Q86bq7 drosophila	946	102	4.9	350	2	Q8MS24	O15338 homo sapien
874	104.5	5.0	2693	2	Q8ISF7	Q8isf3 caenorhabd1	947	102	4.9	357	2	O15338	P78410 homo sapien
875	104.5	5.0	2708	2	Q8ISF4	Q8isf4 caenorhabd1	948	102	4.9	359	2	P78410	O35947 meosocricetu
876	104.5	5.0	2708	2	Q8ISF6	Q8isf6 caenorhabd1	949	102	4.9	461	2	Q35947	Q6nna1 drosophila
877	104.5	5.0	18519	2	Q8ISF7	Q8isf7 caenorhabd1	950	102	4.9	504	2	Q6NNM1	Q9vgd2 drosophila
878	104	5.0	299	1	ALC_RABIT	P01879 oryctolagus	951	102	4.9	508	2	Q9VGD2	O00480 homo sapien
879	104	5.0	334	2	Q9NR44	Q9nr44 homo sapien	952	102	4.9	523	2	O00480	P20916 homo sapien
880	104	5.0	524	1	BUTY_MOUSE	Q62556 mus musculus	953	102	4.9	626	1	MAG_HUMAN	Q9vgd3 drosophila
881	104	5.0	524	2	Q921K7	Q921k7 mus musculus	954	102	4.9	664	2	Q9VGD3	P06731 homo sapien
882	104	5.0	600	2	Q8N7W7	Q8n7w7 homo sapien	955	102	4.9	702	1	CEAS_HUMAN	Q8n4d0 homo sapien
883	104	5.0	662	1	NRG1_RAT	P43322 r pro-neure	956	102	4.9	702	2	Q8N4D0	Q8sqd3 trichosurus
884	104	5.0	694	2	Q8SWT7	Q8swt7 drosophila	957	102	4.9	733	2	Q8SQ83	Q8ctt9 methanosarc
885	104	5.0	734	2	Q96IA4	Q96ia4 homo sapien	958	102	4.9	883	2	O8TTT9	Q8axz4 brachydanio
886	104	5.0	740	2	Q96P29	Q96p29 homo sapien	959	102	4.9	1032	2	Q8AXZ4	Q96ld6 drosophila
887	104	5.0	812	2	Q69ZJ6	Q69zj6 mus musculus	960	102	4.9	1098	2	Q96ID6	Q7tmz9 rattus norv
888	104	5.0	994	1	MERRK_RAT	P57097 rattus norv	961	102	4.9	1249	2	Q7TMZ9	Q906m8 gallus gall
889	104	5.0	998	2	Q9W4Y6	Q9w4y6 drosophila	962	102	4.9	1271	1	MYPC_CHICK	Q9bn17 drosophila
890	104	5.0	1356	1	VGR2_HUMAN	P35968 homo sapien	963	102	4.9	1332	2	Q9BN17	Q9vqw7 drosophila
891	103.5	4.9	147	2	Q8CFJ3	Q8cfj3 mus musculus	964	102	4.9	1332	2	Q9VQW7	Q26438 hyalophora
892	103.5	4.9	275	2	Q9BDN9	Q9bdn9 papilio anubi	965	101.5	4.8	323	2	Q9BDM9	Q9j2m8 rhesus monk
893	103.5	4.9	280	2	Q8UWK1	Q8uwk1 ictalurus p	966	101.5	4.8	413	2	Q26438	Q7z3m6 homo sapien
894	103.5	4.9	287	2	Q9QW80	Q9qw80 mus sp. . f	967	101.5	4.8	423	2	Q9J2M8	Q9vnm6 drosophila
895	103.5	4.9	356	1	HP11_MOUSE	Q9gup5 mus musculus	968	101.5	4.8	520	2	Q7Z3M6	Q9es86 rattus norv
896	103.5	4.9	376	2	Q9QW78	Q9qw78 mus sp. . f	969	101.5	4.8	606	2	Q9VMN6	Q96p30 homo sapien
897	103.5	4.9	413	2	Q639P0	Q639p0 antheraea p	970	101.5	4.8	624	2	Q9ESS6	Q8n6s2 homo sapien
898	103.5	4.9	592	2	Q9JLNS	Q9jln5 mus musculus	971	101.5	4.8	639	2	Q8N6S2	Q8tda0 homo sapien
899	103.5	4.9	628	1	LU_HUMAN	P50895 homo sapien	972	101.5	4.8	742	2	Q8TDA0	P22648 echistocerc
900	103.5	4.9	628	2	Q86VC7	Q86vc7 homo sapien	973	101.5	4.8	802	2	Q8TDA0	Q28730 oryctolagus
901	103.5	4.9	677	1	NRG1_XENLA	Q93383 xenopus lae	974	101.5	4.8	912	1	FAS2_SCHAM	P79921 xenopus lae
902	103.5	4.9	799	2	Q8C3V5	Q8c3v5 mus musculus	975	101.5	4.8	912	2	ICAS2_RABIT	Q66k08 mus musculus
903	103.5	4.9	799	2	Q8CIB8	Q8cib8 mus musculus	976	101.5	4.8	1005	1	P79921	Q7tpv3 mus musculus
904	103.5	4.9	824	2	Q91286	Q91286 pleurodeles	977	101.5	4.8	1184	2	Q66K08	Q6zqa6 mus musculus
905	103.5	4.9	847	1	CD22_HUMAN	P20273 homo sapien	978	101.5	4.8	1194	2	Q7TPV3	Q8bv01 mus musculus
906	103.5	4.9	998	2	Q95RZ7	Q95r27 drosophila	979	101.5	4.8	1214	2	Q6ZQA6	
907	103.5	4.9	1030	2	Q8NFA8	Q8nfa8 homo sapien	980	101.5	4.8	1250	2	Q8BV01	

981	101.5	4.8	1260	1	CAML_MOUSE	P11627	mus musculus	1054	99.5	4.7	500	2	Q9W260	Q9w260 drosophila
982	101.5	4.8	1450	2	Q7QCP2	Q7qcp2 anopheles g	1055	99.5	4.7	549	2	Q6PFC5	Q6pfc5 mus musculus	
983	101.5	4.8	1526	2	Q94538	Q94538 drosophila	1056	99.5	4.7	738	2	P79390	P79390 bos primige	
984	101	4.8	298	2	Q9GL74	Q9gl74 cercopithec	1057	99.5	4.7	821	1	TRKB_MOUSE	P15209 mus musculus	
985	101	4.8	300	2	Q8BEK0	Q8bek0 cowpox viru	1058	99.5	4.7	939	2	Q9VH85	Q9vh85 drosophila	
986	101	4.8	327	2	Q6PCB8	Q6pcb8 homo sapien	1059	99.5	4.7	1009	2	Q93250	Q93250 xenopus lae	
987	101	4.8	478	2	Q661Q4	Q661q4 xenopus lae	1060	99.5	4.7	1019	2	Q8BJK6	Q8bjk6 mus musculus	
988	101	4.8	507	2	Q96K90	Q96k90 homo sapien	1061	99.5	4.7	1021	2	Q93033	Q93033 homo sapien	
989	101	4.8	584	2	Q90989	Q90989 gallus gall	1062	99.5	4.7	1028	2	Q62682	Q62682 rattus norv	
990	101	4.8	605	2	Q8TBU0	Q8tbu0 homo sapien	1063	99.5	4.7	1031	2	Q80YN7	Q80yn7 mus musculus	
991	101	4.8	620	1	SMP_COTJA	Q92154 coturnix co	1064	99.5	4.7	1252	2	Q9JL11	Q9jil1 mus musculus	
992	101	4.8	626	2	Q90880	Q90880 gallus gall	1065	99.5	4.7	1256	2	Q9JIX1	Q9jix1 mus musculus	
993	101	4.8	648	2	Q9BPF1	Q9epf1 mus musculu	1066	99.5	4.7	1379	2	P79701	P79701 coturnix co	
994	101	4.8	673	2	Q6MZW2	Q6mzw2 homo sapien	1067	99.5	4.7	1569	2	Q6PAC0	Q6pac0 mus musculu	
995	101	4.8	693	2	Q9UPU1	Q9upul homo sapien	1068	99.5	4.7	1666	1	MYM1_MOUSE	Q62234 mus musculu	
996	101	4.8	700	1	KIR2_MOUSE	Q7tsu7 mus musculu	1069	99.5	4.7	2021	2	Q62191	Q62191 caenorhabdi	
997	101	4.8	701	2	Q670J1	Q670j1 homo sapien	1070	99.5	4.7	6084	2	Q87ID8	Q87id8 vibrio para	
998	101	4.8	713	2	Q90330	Q90330 coturnix co	1071	99	4.7	234	2	Q8IZQ9	Q8izq9 homo sapien	
999	101	4.8	743	2	Q6P1M7	Q6p1m7 homo sapien	1072	99	4.7	275	1	V055_FOWPV	P21975 fowlpox vir	
1000	101	4.8	890	1	TYO3_HUMAN	Q06418 homo sapien	1073	99	4.7	275	2	Q70H96	Q70h96 fowlpox vir	
1001	101	4.8	892	2	Q86VR3	Q86vr3 homo sapien	1074	99	4.7	313	2	Q35531	Q35531 variola vir	
1002	101	4.8	892	2	P91644	P91644 drosophila	1075	99	4.7	313	2	Q89197	Q89197 mus musculu	
1003	101	4.8	1040	2	Q9W675	Q9w675 brachydanio	1076	99	4.7	359	1	HPL3_MOUSE	Q80wm5 mus musculu	
1004	101	4.8	1214	2	Q75054	Q75054 homo sapien	1077	99	4.7	458	1	CD4_HUMAN	P01730 homo sapien	
1005	101	4.8	1375	2	Q94537	Q94537 drosophila	1078	99	4.7	542	2	Q8NHN5	Q8nhn5 homo sapien	
1006	101	4.8	1944	2	Q695L3	Q695l3 brachydanio	1079	99	4.7	621	2	Q811T7	Q811t7 mus musculu	
1007	101	4.8	3287	2	Q7S9K4	Q7s9k4 neurospora	1080	99	4.7	648	2	Q8R2Y2	Q8r2y2 mus musculu	
1008	101	4.8	6620	2	Q96AA2	Q96aa2 homo sapien	1081	99	4.7	756	2	Q800Z0	Q800z0 brachydanio	
1009	100.5	4.8	280	2	Q8UWL1	Q8uwl1 ictalurus p	1082	99	4.7	773	2	Q9NSW7	Q9nsw7 homo sapien	
1010	100.5	4.8	288	2	Q22385	Q22385 caenorhabdi	1083	99	4.7	812	1	FGRI_XENLA	P22182 xenopus lae	
1011	100.5	4.8	333	2	Q90Z41	Q90z41 gallus gall	1084	99	4.7	831	2	Q71SY9	Q71sy9 gallus gall	
1012	100.5	4.8	337	2	Q6GLZ7	Q6glz7 xenopus lae	1085	99	4.7	891	2	Q8BRX1	Q8brx1 mus musculu	
1013	100.5	4.8	355	1	HPL1_CHICK	P07354 gallus gall	1086	99	4.7	925	2	Q6CRA6	Q6cra6 kluyveromyc	
1014	100.5	4.8	370	2	Q800Y8	Q800y8 brachydanio	1087	99	4.7	931	2	Q8NFX26	Q8nfx26 homo sapien	
1015	100.5	4.8	413	1	HEMO_HYACE	P25033 hyalophora	1088	99	4.7	997	2	Q7PXX0	Q7pxx0 anopheles g	
1016	100.5	4.8	455	2	Q9UIR0	Q9uir0 homo sapien	1089	99	4.7	1345	2	Q8VCD0	Q8vcd0 mus musculu	
1017	100.5	4.8	500	2	Q9XZB7	Q9xzb7 drosophila	1090	99	4.7	1367	1	VGR2_MOUSE	P35918 mus musculu	
1018	100.5	4.8	525	2	Q7OJK5	Q7qjk5 anopheles g	1091	99	4.7	1485	2	Q6A031	Q6a031 mus musculu	
1019	100.5	4.8	606	2	Q9BSS7	Q9bs8 mus musculu	1092	99	4.7	279	2	Q9UD50	Q9ud50 homo sapien	
1020	100.5	4.8	700	1	MEPB_HUMAN	Q16820 homo sapien	1093	98.5	4.7	283	2	Q7QGT4	Q7qgt4 anopheles g	
1021	100.5	4.8	802	1	FGR4_HUMAN	P22455 homo sapien	1094	98.5	4.7	285	2	Q7ZXY30	Q7zy30 xenopus lae	
1022	100.5	4.8	814	2	Q8EC41	Q8ec41 shewanella	1095	98.5	4.7	309	2	Q7QYN57	Q7qyn57 vaccinia vi	
1023	100.5	4.8	876	2	Q7PW78	Q7pw78 anopheles g	1096	98.5	4.7	316	2	Q7Q0P9	Q7q0p9 anopheles g	
1024	100.5	4.8	906	2	Q8TFY9	Q8tfy9 methanosarc	1097	98.5	4.7	413	1	HEMO_MANSE	Q741a5 mycobacteri	
1025	100.5	4.8	1250	2	Q88971	Q88971 mus musculu	1098	98.5	4.7	482	2	Q741A5	Q741a5 mycobacteri	
1026	100.5	4.8	1252	2	Q9EQS9	Q9eqs9 mus musculu	1099	98.5	4.7	611	2	Q8CVC7	Q8cvc7 streptococc	
1027	100.5	4.8	1253	2	Q9EQS8	Q9eqs8 mus musculu	1100	98.5	4.7	1333	1	VGRI_MOUSE	P35969 mus musculu	
1028	100	4.8	307	2	Q94431	Q94431 ciona intes	1101	98.5	4.7	1817	2	Q8TI59	Q8ti59 methanosarc	
1029	100	4.8	314	2	Q8BEK7	Q8bek7 vaccinia vi	1102	98.5	4.7	299	2	Q7Q863	Q7q863 anopheles g	
1030	100	4.8	322	1	ICOL_MOUSE	Q9jih8 mus musculu	1103	98	4.7	302	1	ICOL_HUMAN	Q75144 homo sapien	
1031	100	4.8	329	1	CD86_HUMAN	P42081 homo sapien	1104	98	4.7	347	2	Q9H730	Q9h730 homo sapien	
1032	100	4.8	329	2	Q9TTF2	Q9ttf2 canis famil	1105	98	4.7	381	2	Q9Y4A4	Q9y4a4 homo sapien	
1033	100	4.8	354	1	HPL1_HUMAN	P10915 homo sapien	1106	98	4.7	394	2	Q8HXR7	Q8hxr7 macaca fasc	
1034	100	4.8	400	2	Q8C5E4	Q8c5e4 mus musculu	1107	98	4.7	394	2	Q8HXR9	Q8hxr9 macaca mula	
1035	100	4.8	458	1	CD4_PANTR	P16004 pan troglod	1108	98	4.7	413	2	Q8BGB4	Q8bgb4 m mus mescu	
1036	100	4.8	493	2	Q6P5Y4	Q6p5y4 homo sapien	1109	98	4.7	417	2	Q7TML1	Q7tnl1 mus musculu	
1037	100	4.8	504	2	Q98923	Q98923 gallus gall	1110	98	4.7	492	2	Q7QD44	Q7qd44 anopheles g	
1038	100	4.8	584	2	Q00478	Q00478 homo sapien	1111	98	4.7	569	2	Q8AXU1	Q8axu1 oncorhynch	
1039	100	4.8	584	2	Q98921	Q98921 gallus gall	1112	98	4.7	589	2	Q8R366	Q8r366 mus musculu	
1040	100	4.8	626	2	Q98922	Q98922 gallus gall	1113	98	4.7	628	2	Q9MZ08	Q9mz08 bos taurus	
1041	100	4.8	669	2	Q6B515	Q6b515 poephila gu	1114	98	4.7	645	2	Q6DR98	Q6dr98 mus musculu	
1042	100	4.8	684	2	Q7SEG1	Q7segl neurospora	1115	98	4.7	697	1	SILA_HUMAN	Q961c7 homo sapien	
1043	100	4.8	734	2	Q96P31	Q96p31 homo sapien	1116	98	4.7	824	1	MLT1_HUMAN	Q9udy8 homo sapien	
1044	100	4.8	784	2	Q8I063	Q8i063 drosophila	1117	98	4.7	847	2	Q8N475	Q8n475 homo sapien	
1045	100	4.8	818	1	TRKB_CHICK	Q91987 gallus gall	1118	98	4.7	850	2	Q9ULF7	Q9ulf7 homo sapien	
1046	100	4.8	842	1	UNSA_HUMAN	Q6zn44 homo sapien	1119	98	4.7	880	1	TYO3_MOUSE	P55144 mus musculu	
1047	100	4.8	894	2	Q9VKG1	Q9vkg1 drosophila	1120	98	4.7	880	1	Q6NZM6	P55146 rattus norv	
1048	100	4.8	1014	2	Q8NFA6	Q8nfa6 homo sapien	1121	98	4.7	880	2	Q6NZM6	Q6nzm6 mus musculu	
1049	99.5	4.7	295	2	Q9GL75	Q9gl75 bos taurus	1122	98	4.7	891	1	Q9OY74	Q9oy74 mus musculu	
1050	99.5	4.7	416	2	Q96360	Q96360 hyphancrtria	1123	98	4.7	931	1	UN5C_CHICK	Q7tc25 gallus gall	
1051	99.5	4.7	432	2	Q6DDE7	Q6dde7 xenopus lae	1124	98	4.7	945	2	Q7589	Q7589 equus cabal	
1052	99.5	4.7	459	1	CD4_RABIT	P46630 coryctolagus	1125	98	4.7	1499	2	Q90815	Q90815 gallus gall	
1053	99.5	4.7	476	2	Q80WU0	Q80wu0 mus musculu	1126	98	4.7					

1127	98	4.7	1878	2	Q6CPZ4	Q6cpz4 kluyveromyc	1200	97	4.6	1860	2	Q7PQF4	Q7pqf4 anopheles g
1128	98	4.7	1896	2	Q9IAJ1	Q9iaj1 xenopus lae	1201	96.5	4.6	187	2	Q8K4E4	Q8k4e4 mus musculus
1129	97.5	4.6	210	2	Q7PVL9	Q7pvl9 anopheles g	1202	96.5	4.6	193	2	Q7QGT6	Q7qgt6 anopheles g
1130	97.5	4.6	257	2	Q6NW92	Q6nw92 brachydanio	1203	96.5	4.6	313	2	Q85407	Q85407 varicola maj
1131	97.5	4.6	261	2	Q9W6V1	Q9w6v1 gallus gall	1204	96.5	4.6	313	2	Q8AYZ7	Q8ayz7 variola vir
1132	97.5	4.6	262	2	Q80T70	Q80t70 mus musculus	1205	96.5	4.6	352	2	Q9W6V2	Q9w6v2 gallus gall
1133	97.5	4.6	276	2	Q640S5	Q640s5 xenopus tro	1206	96.5	4.6	385	2	Q9UQF5	Q9uqf5 homo sapien
1134	97.5	4.6	313	2	Q90Z91	Q90z91 brachydanio	1207	96.5	4.6	404	2	Q9UQF5	Q9uqf5 homo sapien
1135	97.5	4.6	316	2	Q8BEK1	Q8bek1 compox vltu	1208	96.5	4.6	510	2	Q7L3E9	Q7l3e9 homo sapien
1136	97.5	4.6	354	1	HPL1_BOVIN	P55252 bos taurus	1209	96.5	4.6	625	2	Q7KMS6	Q7kws6 dictyostell
1137	97.5	4.6	354	1	HPL1_PIG	P10859 sus scrofa	1210	96.5	4.6	772	2	Q9Y2J6	Q9y2j6 homo sapien
1138	97.5	4.6	418	2	Q9EPN5	Q9epn5 hydrochoeru	1211	96.5	4.6	800	2	Q86LF9	Q86lf9 drosophila
1139	97.5	4.6	457	1	CD4_SALISC	Q29037 salimiri sci	1212	96.5	4.6	801	2	Q86LF8	Q86lf8 drosophila
1140	97.5	4.6	457	2	Q8HZT7	Q8hzt7 salimiri sci	1213	96.5	4.6	804	2	Q800Z1	Q800z1 brachydanio
1141	97.5	4.6	462	2	Q06840	Q06840 prevotella	1214	96.5	4.6	806	2	Q90Z00	Q90z00 brachydanio
1142	97.5	4.6	473	2	Q83HS2	Q83hs2 tropheryma	1215	96.5	4.6	836	2	Q8TBZ1	Q8tbz1 homo sapien
1143	97.5	4.6	473	2	Q83MX5	Q83mx5 tropheryma	1216	96.5	4.6	893	2	Q8NDN5	Q8ndn5 strongyloce
1144	97.5	4.6	510	2	Q6EH12	Q6eh12 rattus norv	1217	96.5	4.6	1200	1	HYAL_STRPU	Q76536 strongyloce
1145	97.5	4.6	534	2	Q86SE4	Q86se4 homo sapien	1218	96.5	4.6	1210	1	H1K1_HUMAN	Q86z02 homo sapien
1146	97.5	4.6	534	2	Q866T2	Q866t2 pan troglod	1219	96.5	4.6	1232	2	Q8TCG8	Q8tcg8 homo sapien
1147	97.5	4.6	553	2	Q8WXJ5	Q8wxj5 homo sapien	1220	96.5	4.6	1270	1	MYPC_MOUSE	Q70468 mus musculus
1148	97.5	4.6	571	2	Q8SPI8	Q8spi8 sus scrofa	1221	96.5	4.6	1304	2	Q9VBE5	Q9vbe5 drosophila
1149	97.5	4.6	764	1	ICCR_DROME	Q08180 drosophila	1222	96.5	4.6	1421	2	Q8RT04	Q8rt04 corynebacte
1150	97.5	4.6	764	2	Q8MOQ1	Q8mqg1 drosophila	1223	96.5	4.6	1560	1	TENN_MOUSE	Q80z71 mus musculus
1151	97.5	4.6	764	2	Q9W4U1	Q9w4u1 drosophila	1224	96.5	4.6	2013	2	Q8Y9T8	Q8y9tc8 listeria mo
1152	97.5	4.6	778	1	KIR3_HUMAN	Q81z9 homo sapien	1225	96.5	4.6	3198	2	Q7PVK5	Q7pvk5 manduca sex
1153	97.5	4.6	778	1	KIR3_MOUSE	Q8br86 mus musculus	1226	96	4.6	228	2	Q7PVK5	Q7pvk5 anopheles g
1154	97.5	4.6	822	1	TRKB_HUMAN	Q16620 homo sapien	1227	96	4.6	234	2	Q9MCS7	Q9mc87 bacterioph
1155	97.5	4.6	838	2	Q8WXJ7	Q8wxj7 homo sapien	1228	96	4.6	236	2	Q8P5S3	Q8p5s3 mus musculus
1156	97.5	4.6	876	2	Q78E87	Q78e87 mus musculus	1229	96	4.6	252	2	Q8MLI2	Q8ml12 drosophila
1157	97.5	4.6	931	1	UN5C_HUMAN	Q95185 homo sapien	1230	96	4.6	310	2	Q7QK35	Q7qk35 anopheles g
1158	97.5	4.6	1254	1	Q674V1	Q674v1 podocoryne	1231	96	4.6	310	2	Q8BEI7	Q8bei7 vaccinia vi
1159	97.5	4.6	1348	2	Q8YA37	Q8ya37 listeria mo	1232	96	4.6	312	2	Q8BEJ2	Q8bej2 rabdipox v
1160	97.5	4.6	1383	2	Q7Q840	Q7q840 anopheles g	1233	96	4.6	360	2	Q8N732	Q8n732 homo sapien
1161	97.5	4.6	1443	1	NEO1_CHICK	Q90610 gallus gall	1234	96	4.6	407	1	CD33_HUMAN	P20138 homo sapien
1162	97.5	4.6	1526	2	Q9V6D5	Q9v6d5 drosophila	1235	96	4.6	441	2	GLC2_VIBCH	Q9klp4 vibrio chol
1163	97.5	4.6	5327	1	MACF_MOUSE	Q9qxz0 mus musculus	1236	96	4.6	441	1	Q9DDC4	Q9ddc4 oncorhynch
1164	97	4.6	240	2	Q8WUK3	Q8wuk3 homo sapien	1237	96	4.6	570	2	Q6GMZ9	Q6gmz9 xenopus lae
1165	97	4.6	279	2	Q7TST0	Q7tst0 mus musculus	1238	96	4.6	610	2	Q8RR31	Q8rr31 vibrio fluv
1166	97	4.6	280	2	Q8UWL2	Q8uwl2 ictalurus p	1239	96	4.6	619	2	Q7PXT0	Q7pxt0 anopheles g
1167	97	4.6	294	2	Q8BH36	Q8bh36 mesocricetu	1240	96	4.6	732	2	Q8CWA4	Q8caw4 mus musculus
1168	97	4.6	304	2	Q9BE26	Q9be26 macaca fasc	1241	96	4.6	739	1	VCA1_MOUSE	P29533 mus musculus
1169	97	4.6	305	2	Q7PR66	Q7pr66 anopheles g	1242	96	4.6	739	2	Q91X98	Q91x98 mus musculus
1170	97	4.6	307	2	Q66607	Q66607 equid herpe	1243	96	4.6	771	2	Q8NLI6	Q8nli6 homo sapien
1171	97	4.6	310	2	Q8BEI8	Q8bei8 vaccinia vi	1244	96	4.6	802	2	Q95ML3	Q95ml3 bos taurus
1172	97	4.6	317	2	Q8BEK2	Q8bek2 compox viru	1245	96	4.6	1016	2	Q7JFL6	Q7jfl6 oryctolagus
1173	97	4.6	388	2	Q8NFZ8	Q8nfz8 homo sapien	1246	96	4.6	1035	2	Q9NEG1	Q9neg1 drosophila
1174	97	4.6	393	2	Q8HXR8	Q8hxr8 cercopithec	1247	96	4.6	1043	2	Q6PA07	Q6pa07 xenopus lae
1175	97	4.6	456	2	Q7PUM9	Q7pum9 anopheles g	1248	96	4.6	1193	2	Q9VQW1	Q9vqw1 drosophila
1176	97	4.6	472	2	Q6AF32	Q6af32 leifsonia x	1249	96	4.6	1294	2	Q80TBO	Q80tb0 mus musculus
1177	97	4.6	495	1	A1BG_HUMAN	P04217 homo sapien	1250	96	4.6	1294	2	Q977Y4	Q977y4 clostridium
1178	97	4.6	508	2	Q8BJA5	Q8bjas mus musculus	1251	96	4.6	1483	2	Q82YWB	Q82yw8 enterococcu
1179	97	4.6	697	2	Q8TC35	Q8tc35 homo sapien	1252	96	4.6	1744	1	PGS2_RAT	Q00657 oryctolagus
1180	97	4.6	703	2	Q65XY2	Q65xy2 caenorhabdi	1253	96	4.6	2326	2	Q28733	Q28733 oryctolagus
1181	97	4.6	724	1	Q8MXU5	Q8mxus caenorhabdi	1254	96	4.6	6875	2	Q7PXF7	Q7pxf7 anopheles g
1182	97	4.6	739	1	VCA1_HUMAN	P19320 homo sapien	1255	95.5	4.6	220	2	CD48_HUMAN	P09326 homo sapien
1183	97	4.6	740	1	PEC1_PIG	Q95242 sus scrofa	1256	95.5	4.6	243	1	Q61AZ2	Q61az2 homo sapien
1184	97	4.6	751	2	Q39294	Q39294 equid herpe	1257	95.5	4.6	243	2	Q6QVZ1	Q6qvz1 aracatuba v
1185	97	4.6	804	2	Q8WV47	Q8wv47 homo sapien	1258	95.5	4.6	308	2	Q91ZR9	Q91zr9 cantagalo o
1186	97	4.6	821	2	Q8BFT0	Q8bft0 m mus muscu	1259	95.5	4.6	308	2	Q8R464	Q8r464 mus musculus
1187	97	4.6	824	2	Q90749	Q90749 gallus gall	1260	95.5	4.6	388	2	Q9NPPE	Q9npp6 homo sapien
1188	97	4.6	891	2	Q9UHW6	Q9uhw6 homo sapien	1261	95.5	4.6	416	2	IRL1_HUMAN	Q01638 homo sapien
1189	97	4.6	949	1	MDC1_RAT	P60756 rattus norv	1262	95.5	4.6	556	1	Q6GN50	Q6gn50 xenopus lae
1190	97	4.6	994	1	MERK_MOUSE	Q07409 mus musculus	1263	95.5	4.6	573	2	Q9UQL3	Q9uql3 homo sapien
1191	97	4.6	1028	2	Q07409	P29294 oryctolagus	1264	95.5	4.6	591	2	Q86X29	Q86x29 homo sapien
1192	97	4.6	1147	1	KMLS_RABIT	Q95YK1 ciona savig	1265	95.5	4.6	601	2	Q70W32	Q70w32 oncorhynch
1193	97	4.6	1177	2	Q95YK1	Q6r2f7 homo sapien	1266	95.5	4.6	643	1	LIB5_PANTR	Q8mjz7 pan troglod
1194	97	4.6	1273	2	Q6R2F7	Q14896 homo sapien	1267	95.5	4.6	648	2	Q8F6A9	Q8f6a9 leptospiro
1195	97	4.6	1274	1	MYPC_HUMAN	Q9um53 homo sapien	1268	95.5	4.6	692	2	Q800Y9	Q800y9 brachydanio
1196	97	4.6	1274	2	Q9UM53	Q9um53 homo sapien	1269	95.5	4.6	692	2	Q922E0	Q922e0 mus musculus
1197	97	4.6	1321	2	Q75129	Q75129 homo sapien	1270	95.5	4.6	727	1	PEC1_MOUSE	Q08481 mus musculus
1198	97	4.6	1375	2	Q8ML47	Q8ml47 drosophila	1271	95.5	4.6	757	2	Q7QCT0	Q7qcu0 anopheles g
1199	97	4.6	1535	2	Q23991	Q23991 drosophila	1272	95.5	4.6				

1273	95.5	4.6	808	2	Q7PVZ3	Q7pvz3 anopheles g	1346	94	4.5	583	2	Q8VZR7	Q8vzr7 arabidopsis
1274	95.5	4.6	816	2	Q8IYD7	Q8iyd7 homo sapien	1347	94	4.5	602	2	Q9VFD9	Q9vfd9 drosophila
1275	95.5	4.6	879	2	Q8VI99	Q8vi99 rattus norv	1348	94	4.5	943	2	Q30320	Q30320 archaeglob
1276	95.5	4.6	887	2	Q8YWI7	Q8ywi7 anabaena sp	1349	94	4.5	1010	1	CONT_CHICK	P14781 gallus gall
1278	95.5	4.6	888	2	Q8VIA0	Q8via0 rattus norv	1350	94	4.5	1280	2	Q9EPX2	Q9epx2 mus musculu
1279	95.5	4.6	1131	1	MYPF_CHICK	P16419 gallus gall	1351	94	4.5	1325	1	YDEK_ECOLI	P32051 escherichia
1280	95.5	4.6	1163	2	Q94HMS	Q94hms oryza sativ	1352	94	4.5	1406	2	Q9GPF7	Q9gpf7 drosophila
1281	95.5	4.6	1163	2	Q7XG19	Q7xg19 oryza sativ	1353	94	4.5	1463	2	Q9VQ08	Q9vq08 drosophila
1282	95.5	4.6	1242	1	NPHN_MOUSE	Q9qz87 mus musculu	1354	94	4.5	1648	2	Q12275	Q12275 saccharomyc
1283	95.5	4.6	1264	2	P91767	P91767 manduca sex	1355	94	4.5	1945	2	Q9V491	Q9v491 drosophila
1284	95.5	4.6	1948	1	PTNS_HUMAN	Q13332 homo sapien	1356	94	4.5	13133	2	Q71A42	Q71a42 caenorhabdi
1285	95	4.5	181	2	Q91665	Q91665 xenopus lae	1357	93.5	4.5	259	2	Q8UVA5	Q8uva5 brachydanio
1286	95	4.5	229	2	Q7PVL3	Q7pvl3 anopheles g	1358	93.5	4.5	261	2	Q8AUQ4	Q8auq4 brachydanio
1287	95	4.5	252	2	Q9CX63	Q9cx63 mus musculu	1359	93.5	4.5	296	2	Q42404	Q42404 gallus gall
1287	95	4.5	270	2	O00426	O00426 homo sapien	1360	93.5	4.5	313	2	Q8UV33	Q8uv33 brachydanio
1288	95	4.5	312	2	Q8BEJ3	Q8bej3 rabbitpox v	1361	93.5	4.5	315	2	Q6UN41	Q6un41 cowpox viru
1289	95	4.5	330	2	Q8C2J8	Q8c2j8 mus musculu	1362	93.5	4.5	326	2	Q8UV70	Q8uv70 brachydanio
1290	95	4.5	343	2	Q6U7R4	Q6u7r4 mus musculu	1363	93.5	4.5	330	1	CD86_RABIT	P42071 oryctolagus
1291	95	4.5	362	2	Q8C1C7	Q8c1c7 mus musculu	1364	93.5	4.5	332	2	Q95LI6	Q95li6 felis silve
1292	95	4.5	388	2	Q92151	Q92151 mus musculu	1365	93.5	4.5	332	2	Q9GMZ7	Q9gmz7 felis silve
1293	95	4.5	405	2	Q6PFK4	Q6pfk4 brachydanio	1366	93.5	4.5	336	2	Q8WVW5	Q8wvw5 homo sapien
1294	95	4.5	438	2	Q920C3	Q920c3 mus musculu	1367	93.5	4.5	379	2	Q9CWM1	Q9cwm1 mus musculu
1295	95	4.5	457	2	Q960D1	Q960d1 drosophila	1368	93.5	4.5	492	2	Q9ET54	Q9et54 mus musculu
1296	95	4.5	509	1	SHS1_RAT	P97710 r protein-t	1369	93.5	4.5	510	2	Q801V8	Q801v8 brachydanio
1297	95	4.5	521	1	C166_RABIT	Q46651 oryctolagus	1370	93.5	4.5	655	2	Q8A9U5	Q8a9u5 bacterioides
1298	95	4.5	739	1	PECI_BOVIN	P51866 bos taurus	1371	93.5	4.5	729	1	FGR1_DROME	Q07407 drosophila
1299	95	4.5	814	2	Q8IVU1	Q8ivul homo sapien	1372	93.5	4.5	808	1	FGR4_MOUSE	Q03142 mus musculu
1300	95	4.5	814	2	Q91897	Q91897 xenopus lae	1373	93.5	4.5	853	2	Q6DFX7	Q6dfx7 mus musculu
1301	95	4.5	847	2	Q8BFR2	Q8bfr2 m mus muscu	1374	93.5	4.5	1038	2	Q42480	Q42480 xenopus lae
1302	95	4.5	847	2	Q8C4T3	Q8c4t3 mus musculu	1375	93.5	4.5	1210	2	Q6BLQ0	Q6bliq0 debaryomyc
1303	95	4.5	949	1	MDC1_MOUSE	P60755 mus musculu	1376	93.5	4.5	1264	2	O14631	O14631 homo sapien
1304	95	4.5	1052	2	Q7PMY4	Q7pmY4 anopheles g	1377	93.5	4.5	1630	2	Q90724	Q90724 gallus gall
1305	95	4.5	1371	2	Q8BV57	Q8bv57 mus musculu	1378	93.5	4.5	3396	1	PGCV_HUMAN	P13611 homo sapien
1306	95	4.5	1450	1	MPSF_CHICK	Q02173 gallus gall	1379	93	4.4	280	2	Q8UV51	Q8uv51 brachydanio
1307	95	4.5	1501	2	Q7TT17	Q7tt17 mus musculu	1380	93	4.4	308	2	Q9IC17	Q9ic17 vaccinia vi
1308	95	4.5	1501	2	Q9QW00	Q9qw00 rattus sp.	1381	93	4.4	330	1	EMB_MOUSE	P21995 mus musculu
1309	95	4.5	1527	2	Q9VZZ4	Q9vzz4 drosophila	1382	93	4.4	333	2	Q7PXA4	Q7pxa4 anopheles g
1310	95	4.5	1863	2	Q64605	Q64605 rattus norv	1383	93	4.4	370	1	C244_HUMAN	Q9bzw8 homo sapien
1311	95	4.5	1898	2	Q9EQ17	Q9eq17 mus musculu	1384	93	4.4	379	2	Q80UL9	Q80ul9 mus musculu
1312	95	4.5	1904	2	Q64699	Q64699 mus musculu	1385	93	4.4	388	1	BASI_RAT	P26453 rattus norv
1313	95	4.5	1945	2	Q96681	Q96681 drosophila	1386	93	4.4	390	2	Q7QBR2	Q7qbr2 anopheles g
1314	95	4.5	22152	2	Q8WX17	Q8wx17 homo sapien	1387	93	4.4	413	2	Q6KDB4	Q6kdb4 escherichia
1315	94.5	4.5	315	1	HEMA_VACCC	P20978 vaccinia vi	1388	93	4.4	424	2	Q8FIX7	Q8fix7 escherichia
1316	94.5	4.5	341	2	Q819K3	Q819k3 branchiosto	1389	93	4.4	435	1	PSG6_HUMAN	Q00889 homo sapien
1317	94.5	4.5	371	2	Q6DCH5	Q6dch5 xenopus lae	1390	93	4.4	459	2	Q6ZMD0	Q6zmd0 homo sapien
1318	94.5	4.5	454	2	Q6MG97	Q6mg97 rattus norv	1391	93	4.4	555	1	C166_CARAU	Q90304 carassius a
1319	94.5	4.5	570	2	Q6GLY1	Q6gly1 xenopus lae	1392	93	4.4	589	2	Q22096	Q22096 caenorhabdi
1320	94.5	4.5	588	1	C166_CHICK	P42292 gallus gall	1393	93	4.4	598	2	Q8BIW7	Q8biw7 m mus muscu
1321	94.5	4.5	593	2	Q6INM5	Q6inm5 xenopus lae	1394	93	4.4	606	2	Q9BZD0	Q9bzd0 homo sapien
1322	94.5	4.5	733	2	Q9QZM7	Q9qzm7 mus musculu	1395	93	4.4	606	2	Q8BZD4	Q8bzd4 m mus muscu
1323	94.5	4.5	755	2	Q8CCF8	Q8ccf8 mus musculu	1396	93	4.4	650	2	Q9GKR2	Q9gkr2 bos taurus
1324	94.5	4.5	868	2	Q86VP2	Q86vf2 homo sapien	1397	93	4.4	719	1	LRFS_MOUSE	Q8bxa0 mus musculu
1325	94.5	4.5	879	2	Q6PE80	Q6pe80 mus musculu	1398	93	4.4	736	2	Q8MY52	Q8mys2 drosophila
1326	94.5	4.5	888	1	UFO_MOUSE	Q00993 mus musculu	1399	93	4.4	739	2	Q9GKR3	Q9gkr3 bos taurus
1327	94.5	4.5	888	2	Q80YQ3	Q80yq3 mus musculu	1400	93	4.4	739	2	Q8K0X1	Q8k0x1 mus musculu
1328	94.5	4.5	931	1	UN5C_MOUSE	O08747 mus musculu	1401	93	4.4	741	2	Q8KTF0	Q8ktf0 listeria mo
1329	94.5	4.5	999	1	MERK_HUMAN	Q12866 homo sapien	1402	93	4.4	774	2	Q9V930	Q9v930 drosophila
1330	94.5	4.5	1083	2	Q76698	Q76698 caenorhabdi	1403	93	4.4	831	2	Q70LU0	Q70lu0 homo sapien
1331	94.5	4.5	1327	2	Q8OHJ3	Q8ghj3 gallus gall	1404	93	4.4	841	2	Q70LT9	Q70lt9 homo sapien
1332	94.5	4.5	1343	1	VGR2_RAT	O08775 rattus norv	1405	93	4.4	848	2	Q25198	Q25198 hydra atten
1333	94.5	4.5	2425	2	Q95M00	Q95mj0 tupaiia glis	1406	93	4.4	1018	2	Q28106	Q28106 bos taurus
1334	94.5	4.5	3029	2	Q7Q767	Q7q767 anopheles g	1407	93	4.4	1021	2	Q9P2X5	Q9p2x5 homo sapien
1335	94	4.5	252	2	Q86PE5	Q86pes drosophila	1408	93	4.4	1025	2	Q9H4E0	Q9h4e0 homo sapien
1336	94	4.5	275	2	Q7PVM4	Q7pvm4 anopheles g	1409	93	4.4	1094	1	DPOD_PLAFK	P30315 plasmodium
1337	94	4.5	313	1	HEMA_VARV	P33807 variola vir	1410	93	4.4	1094	2	Q7KQL4	Q7kql4 plasmodium
1338	94	4.5	313	2	Q8AYW3	Q8ayw3 variola vir	1411	93	4.4	1310	2	Q96RV4	Q96rv4 homo sapien
1339	94	4.5	313	2	Q8BEI4	Q8bei4 variola vir	1412	93	4.4	1337	2	Q9BZA6	Q9bza6 homo sapien
1340	94	4.5	327	2	Q8UV63	Q8uv63 brachydanio	1413	93	4.4	1347	2	Q96RW0	Q96rw0 homo sapien
1341	94	4.5	398	2	Q723B9	Q723b9 homo sapien	1414	93	4.4	1347	2	Q9BZA7	Q9bza7 homo sapien
1342	94	4.5	419	2	Q86M56	Q86m56 drosophila	1415	93	4.4	2738	1	PGCV_RAT	Q9etb4 rattus norv
1343	94	4.5	484	2	Q99JQ8	Q99jq8 mus musculu	1416	93	4.4	3381	1	PGCV_BOVIN	P81282 bos taurus
1344	94	4.5	533	2	Q9DEB5	Q9dees gallus gall	1417	92.5	4.4	243	1	CAVT_BRALA	P05548 branchiosto
1345	94	4.5	583	2	O22889	O22889 arabidopsis	1418	92.5	4.4	245	1	MOG_RAT	Q63345 rattus norv

1419	92.5	4.4	245	2	Q6MPX9	Q6mfx9	rattus norv
1420	92.5	4.4	277	2	Q8C6H8	Q8c6h8	mus musculus
1421	92.5	4.4	281	2	Q8CJEB	Q8cje8	mesocricetu-
1422	92.5	4.4	282	2	Q7Z7D3	Q7z7d3	homo sapien
1423	92.5	4.4	296	2	Q8MMZ2	Q8mmz2	bus scrofa
1424	92.5	4.4	310	2	Q8TQ07	Q8tq07	methanosarc
1425	92.5	4.4	329	2	Q9XSK6	Q9xsk6	felis silve
1426	92.5	4.4	330	2	Q9QZ42	Q9qz42	gallus gall
1427	92.5	4.4	337	2	Q9VJF7	Q9vjf7	drosofila
1428	92.5	4.4	393	2	Q9S727	Q9s727	homo sapien
1429	92.5	4.4	463	2	Q8C1V9	Q8c1v9	mus musculus
1430	92.5	4.4	474	2	Q8K178	Q8k178	mus musculus
1431	92.5	4.4	492	2	Q99KT6	Q99kt6	mus musculus
1433	92.5	4.4	669	2	Q6NNB6	Q6nnb6	drosofila
1433	92.5	4.4	762	2	Q71TW8	Q71tw8	homo sapien
1434	92.5	4.4	763	2	Q9V114	Q9v114	drosofila
1435	92.5	4.4	764	1	P1GR_HUMAN	P01833	homo sapien
1436	92.5	4.4	764	2	Q81ZT7	Q81zy7	homo sapien
1437	92.5	4.4	821	1	TRKB_RAT	Q63604	rattus norv
1438	92.5	4.4	886	2	Q9VM64	Q9vm64	drosofila
1439	92.5	4.4	1053	2	Q6EQM4	Q6eqm4	oryza sativ
1440	92.5	4.4	1078	2	Q6NRQ4	Q6nrq4	xenopus lae
1441	92	4.4	222	2	Q8IX38	Q8ix38	homo sapien
1442	92	4.4	290	2	Q7OCM3	Q7qcm3	anopheles g
1443	92	4.4	293	2	Q8AXN8	Q8axn8	cyprinus ca
1444	92	4.4	305	2	Q98261	Q98261	homo sapien
1445	92	4.4	305	2	Q8VBW0	Q8vbw0	mus musculus
1446	92	4.4	321	2	Q8MY16	Q8my16	ascaris suu
1447	92	4.4	323	1	CD47_HUMAN	Q08722	homo sapien
1448	92	4.4	330	1	CD22_PONPY	Q9n1e3	pongo pygma
1449	92	4.4	330	2	Q8C543	Q8c543	mus musculus
1450	92	4.4	367	2	Q6ZML4	Q6zml4	homo sapien
1451	92	4.4	419	2	Q68C66	Q68cr6	homo sapien
1452	92	4.4	422	2	Q7RTV9	Q7rtv9	homo sapien
1453	92	4.4	454	1	MUC_HUMAN	P01871	homo sapien
1454	92	4.4	485	2	Q801W5	Q801w5	brachydanio
1455	92	4.4	526	2	Q8NG09	Q8ng09	homo sapien
1456	92	4.4	544	2	Q7ZZ85	Q7zz85	brachydanio
1457	92	4.4	564	1	C166_BRARE	Q90460	brachydanio
1458	92	4.4	583	2	Q6IQX4	Q6iqx4	brachydanio
1459	92	4.4	583	1	C166_HUMAN	Q13740	homo sapien
1460	92	4.4	607	2	Q8OVF2	Q8ovf2	mus musculus
1461	92	4.4	613	2	Q969P0	Q969p0	homo sapien
1462	92	4.4	696	1	IPL1_RAT	P59824	rattus norv
1463	92	4.4	700	2	Q9P244	Q9p244	homo sapien
1464	92	4.4	738	2	Q8C6V9	Q8c6v9	mus musculus
1465	92	4.4	826	2	Q7Q1P7	Q7q1p7	anopheles g
1466	92	4.4	876	2	Q8K0J1	Q8k0j1	mus musculus
1467	92	4.4	902	2	Q17576	Q17576	caenorhabdi
1468	92	4.4	928	2	Q9BLV1	Q9blv1	caenorhabdi
1469	92	4.4	931	1	UN5C_RAT	Q761x5	rattus norv
1470	92	4.4	948	2	Q9T7D7	Q9tcd7	trichosurus
1471	92	4.4	956	1	MDCL_HUMAN	Q72553	homo sapien
1472	92	4.4	1282	2	Q8C2F9	Q8c2f9	mus musculus
1473	92	4.4	2483	1	MPRI_MOUSE	Q07113	mus musculus
1474	92	4.4	2491	1	MPRI_HUMAN	P11717	homo sapien
1475	92	4.4	2491	2	Q96PT5	Q96pt5	homo sapien
1476	92	4.4	2491	2	Q7Z7G9	Q7z7g9	homo sapien
1477	92	4.4	12268	2	Q8MQ08	Q8mq08	caenorhabdi
1478	92	4.4	13100	2	Q09165	Q09165	caenorhabdi
1479	91.5	4.4	153	2	Q9R1A2	Q9ria2	mus musculus
1480	91.5	4.4	196	2	Q7PJY5	Q7pjy5	anopheles g
1481	91.5	4.4	234	2	Q6NS95	Q6ns95	homo sapien
1482	91.5	4.4	240	1	CD48_MOUSE	P18181	mus musculus
1483	91.5	4.4	240	2	Q6P905	Q6p905	mus musculus
1484	91.5	4.4	299	2	Q9VHQ8	Q9vhq8	drosofila
1485	91.5	4.4	366	2	Q64216	Q64216	spalax zemn
1486	91.5	4.4	412	2	Q8HXT9	Q8hxt9	colypeutes
1487	91.5	4.4	451	2	Q8VD31	Q8vd31	mus musculus
1488	91.5	4.4	459	2	Q86X91	Q86x91	homo sapien
1489	91.5	4.4	463	2	Q9GMB5	Q9gmb5	bos indicus
1490	91.5	4.4	541	2	Q95XJ7	Q95xj7	caenorhabdi
1491	91.5	4.4	570	2	Q8NCE6	Q8nce6	homo sapien

1492	91.5	4.4	573	2	Q8C6P3	Q8c6p3	mus musculus
1493	91.5	4.4	573	2	Q8C833	Q8c833	mus musculus
1494	91.5	4.4	576	1	IL1R_MOUSE	P13504	mus musculus
1495	91.5	4.4	603	2	Q8VBZ9	Q8vbz9	mus musculus
1496	91.5	4.4	627	2	Q72PX7	Q72px7	leptosira
1497	91.5	4.4	675	2	Q7T0V5	Q7t0v5	xenopus lae
1498	91.5	4.4	789	2	Q8N2P7	Q8n2p7	homo sapien
1499	91.5	4.4	880	2	Q8QFP9	Q8qfp9	xenopus lae
1500	91.5	4.4	906	2	Q8UVU1	Q8uvu1	xenopus lae

ALIGNMENTS

```
RESULT 1
Q9Y279
ID Q9Y279 PRELIMINARY; PRT; 399 AA.
AC Q9Y279;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Z391g protein precursor (V-set and immunoglobulin domain containing
4).
GN Name=Z391g; Synonyms=VSIG4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461865; Pubmed=11004523; DOI=10.1016/S0167-4781(00)00131-7;
RA Langnaese K., Colleaux L., Kloos D.U., Fontes M., Wieacker P.;
RT "Cloning of Z391g, a novel gene with immunoglobulin-like domains
located on human chromosome X.";
RL Biochim. Biophys. Acta 1492:522-525(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132502; CAB51536.1; -.
DR EMBL; BC010525; AAH10525.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL 1 19 Potential.
```

FT CHAIN 20 399 2391g protein.
SQ SEQUENCE 399 AA; 43987 MW; 735CA3BC58185035 CRC64;
Query Match 100.0%; Score 2098; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.5e-157;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTVLVKMLVQR 60
Db 1 MGILLGLLLGLHLLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPPQGMRLISLQCGARSPISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPPQGMRLISLQCGARSPISYIWKQ 180
QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDTTMDGYLGETSAGPGKSLPVFAILLISLCCMVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDTTMDGYLGETSAGPGKSLPVFAILLISLCCMVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
Db 301 MAYIMLCRKTSQOEHVYEAAARAAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNYARLLDTPVLDYEFPLATEGKSVC 399
Db 361 PCIGOEYQIIAQINGNYARLLDTPVLDYEFPLATEGKSVC 399

RESULT 2
Q6UXI4 PRELIMINARY; PRT; 321 AA.
ID Q6UXI4
AC Q6UXI4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE STIGMA.
GN ORFNames=UNQ317;
OS Homo sapiens. (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358341; AAQ8707.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig_2.
DR SMART; SM00408; IGC2; 1.

DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 321 AA; 35544 MW; B2AB2E3151D39C6E CRC64;
Query Match 80.5%; Score 1688; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 7.5e-125;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTVLVKMLVQR 60
Db 1 MGILLGLLLGLHLLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPPQGMRLISLQCGARSPISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPPQGMRLISLQCGARSPISYIWKQ 180
QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDTTMDGYLGETSAGPGKSLPVFAILLISLCCMVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDTTMDGYLGETSAGPGKSLPVFAILLISLCCMVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAAR 321
Db 301 MAYIMLCRKTSQOEHVYEAAAR 321

RESULT 3
Q80WA3 PRELIMINARY; PRT; 280 AA.
ID Q80WA3
AC Q80WA3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein BC025105.
GN Name=BC025105;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;

RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025105; AAH25105.1; -
DR MGD; MGI:2679720; BC025105.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 280 AA; 31467 MW; 3F099AE96CE8977 CRC64;

Query Match 40.0%; Score 840; DB 2; Length 280;
Best Local Similarity 47.4%; Pred. No. 5e-58;
Matches 175; Conservative 37; Mismatches 57; Indels 100; Gaps 3;

QY 1 MGILGLLLGLHLLTVDTYGRPILEVPEESVTGPMKGDVNLPCYYDPLQGYTQVLVKMLVQR 60
D 1 MEISSGLLFLGLHLLVLTGYGHPTLKTPESVTGTMKGDVKIQCTYDPLRGYRQVLVKMLVVRH 60

QY 61 GSDPYTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLSQSLTLEMDDRSHTCEVTWQTP 120
D 61 GSDSVTIFLRDSTGDHIQQAQYRGRHLKVSHPGVDVSLQINTLQMDRNNHTCEVTWQTP 120

QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRISSQCARGSPPISYIWKQ 180
D 121 DGNQVVRDKITELRVKY-----NPP----- 141

QY 181 QTNQEPKIVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSDIVKFWKDSKILKTK 240
D 142 -----RIN 144

QY 241 TEAPPTMTYPLKATSTVKQSWDTTMDGYLGETSAGPGSLPVFAILLISLCMVVFT 300
D 145 TEAPPTLHSLLEATTIMSTSDLTNGTCKLEETIAGSGRNLPFAIIFIISLCCLVAVT 204

QY 301 MAYIMLCRKTSQOEHVYEAPARAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
D 205 IPIYILFRCTFQOEYVYGVSRVAPARKTSNSEETRVTTIA-----TDEPDQSQALISDYSDD 260

QY 361 PCIGQEQYQI 369
D 261 PCISQEQYQI 269

RESULT 4
JAM1_HUMAN STANDARD; PRT; 299 AA.
AC Q9Y6Z4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
molecule 1) (PAM-1) (Platelet F11 receptor) (UNQ264/PRO301).
GN Name=F11R; Synonyms=JAM1, JCAM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323940; PubMed=10395639;
RA Ozaki H., Ishii K., Horikuchi H., Arai H., Kawamoto T., Okawa K.,
RA Iwamatsu A., Kita T.;
RT "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
of junctional adhesion molecule in human endothelial cells.";
RL J. Immunol. 163:553-557 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
RA Kornecki E.;
RT "Molecular cloning and sequencing of the cDNA of F11 receptor, a novel
Ig superfamily member from human platelets.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RA Naik U.P., Naik M.U., Deleon P., Spychala J.;
RT "Cloning and characterization of PAM-1, a novel platelet adhesion
molecule involved in platelet activation.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glaesl S.,
RA Ansoerg W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Foustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [7]
RP SEQUENCE OF 28-42.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";
RL Protein Sci. 13:2819-2824 (2004).
CC -I- FUNCTION: Seems to play a role in epithelial tight junction
formation. Appears early in primordial forms of cell junctions and
recruits PARD3. The association of the PARD6-PARD3 complex may
prevent the interaction of PARD3 with JAM1, thereby preventing
tight junction assembly (By similarity). Plays a role in
regulating monocyte transmigration involved in integrity of
epithelial barrier. Involved in platelet activation.
CC -I- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
association between PARD3 and PARD6 probably disrupts this
interaction (By similarity).


```
CC -| SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -| TISSUE SPECIFICITY: Localized at tight junctions of both
CC epithelial and endothelial cells.
CC -| SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -| SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF111713; AAD42050.1; -.
DR EMBL; AF207907; AAF22829.1; -.
DR EMBL; AF172398; AAD48877.1; -.
DR EMBL; AL136649; CAB66584.1; -.
DR EMBL; AY358896; AAQ89255.1; -.
DR EMBL; BC001533; AAH01533.1; -.
DR PIR; A59406; S56749.
DR PDB; 1NBQ; X-ray; A/B=25-233.
DR Genew; HGNC:14685; F11R.
DR MIM; 605721; -.
DR GO; GO:0005911; C:intercellular junction; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
FT SIGNAL 1 27
FT CHAIN 28 299 Junctional adhesion molecule 1.
FT DOMAIN 28 238 Extracellular (Potential).
FT TRANSMEM 239 259 Potential.
FT DOMAIN 260 299 Cytoplasmic (Potential).
FT DOMAIN 28 125 Ig-like V-type 1.
FT DOMAIN 135 228 Ig-like V-type 2.
FT DISULFID 50 109 Potential.
FT DISULFID 153 212 Potential.
FT CARBOHYD 185 185 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match 8.5%; Score 178.5; DB 1; Length 299;
Best Local Similarity 26.5%; Pred. No. 8.3e-06;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKLVQR 60
   : ||| | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 17 IAILLCSLALGSVTVHS-SEBEVRIPEN-----NPVKLSLAY--SGFSSPRVEW---- 62

QY 61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHK-----VPGDVSLLQLSTLEMDDRSHYTCEV 115
   : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 63 -----KFDQGDPTTRVVCYNNKITASYEDRVTFLEPTGTFKSVTRE--DTGTYTCMV 111

QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPGMRISLQCCQAR-GSPPIIS 174
   : : : : | : | : | : | : | : | : | : | : | : | : | : |
Db 112 SEEGNSYGEVKVLIVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEQDGSPPSE 163

QY 175 YIWK-----QQTN-----NQEPKAVTLSTLFPKPAVIADSGSYFCTAKGVGSEQH 222
   | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 164 YTWFKDGIWPTNPKSTRAFSNSSYVLNPTTGLVFPDLASADTGEYSCEARNGYGTPTMT 223

QY 223 SDIVK 227
   | : | :
Db 224 SNAVR 228
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RESULT 5
Q10465 PRELIMINARY; PRT; 7962 AA.
ID Q10465;
AC Q10465;
DT 01-NOV-1996 (Tremblrel. 01, Created)

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DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Elastic titin (Fragment).
GN Name=titin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Skeletal muscle;
RX MEDLINE=96026330; PubMed=7569978;
RA Label S., Kolmerer B.;
RT "Titins, giant proteins in charge of muscle ultrastructure and
RT elasticity.";
RL Science 270:293-296(1995).
DR EMBL; X90569; CAA62189.1; -.
DR PIR; I38346; I38346.
DR HSSP; P11362; 1EVT.
DR GO; GO:0030017; C:sarcomere; TAS.
DR GO; GO:0008307; F:structural constituent of muscle; TAS.
DR GO; GO:0006941; P:striated muscle contraction; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR004168; PPAK_motif.
DR Pfam; PF02818; PPAK; 53.
DR SMART; SM00408; IGC2; 43.
DR PROSITE; PS50835; IG_LIKE; 58.
FT NON_TER 1 1
FT NON_TER 7962 7962
SQ SEQUENCE 7962 AA; 883018 MW; B85240533CBAD58 CRC64;
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Query Match 8.5%; Score 178; DB 2; Length 7962;
Best Local Similarity 24.2%; Pred. No. 0.00069;
Matches 102; Conservative 56; Mismatches 169; Indels 94; Gaps 20;

QY 16 DTYGRPILEVPES-VTGPWKGDVNLPCITYDPLQGYTQVLVKW-----LVQSGSDP 64
   | : | : | : | | | | | : | : | : | : | : | : | : | : |
Db 860 DSSGALIVQEPSPFVTKPGSKDV-LPGSAVCLKSTFQGSTPLTIRWFKGNKELVSGSCY 918

QY 65 VTIFLRDSSGDHIQAKYQGRHLVSHKVPDVSLLQLSTLEMDDRSHYTCEVTPPDG-- 122
   : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 919 IT-----KEALSSLELYLVKTSDSGTTCYS-NVAGVE 953

QY 123 ---NQVRDKITELRVQKLSVSKPTVTGSGYGFVPGMRISLQCCQARSGSPISYIWK 179
   | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 954 CSANLFVKEPAT--FVEKLEPSQ-----LLKKGDATQLACKVTGTPPIKITWFA 1000

QY 180 QQTNNQEPK-----VATLSTLFPKPAVIADSGSYFCTAKGVGSEQHSDIVKFKVQSS 234
   : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1001 NDREIKESSKRMFVESTAVLRLLTDVGIEISGEYMCQAQNEAGSDHCSSIV--IVKESP 1058

QY 235 -----KLKTKTEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPVEALI 288
   | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1059 YFTKEFKPIEVLKEYDVMLLAEVAGTPPPEITW-----FKDNTILRSGRKYKTFIQD 1110

QY 289 LIISLCM-VVFTWYIMLCRKTSQOEHYVEARAHAAREAN-----DSGETMR--VAIF 339
   : : | : | : | : | : | : | : | : | : | : | : | : |
Db 1111 HLVSLLQLKFVADAGEYQCRVTNEVGSSICSAVTLREPPSFIKKIESYSSLRGTAFA 1170

QY 340 ASGCCSDEPTSQNLGNNSYDEPCIGQEQYQIAQINGNYARL-LDTVPFLDYFLATEGKSV 398
   : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1171 QATLKGLSPITVWMLKD-SDE--ITEDDNIRMTFENNVAASLYLSGIEVGH-----DGKYV 1222

QY 399 C 399
   |
Db 1223 C 1223
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RESULT 6
Q8W242 PRELIMINARY; PRT; 34350 AA.
ID Q8W242;
AC Q8W242;

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; U79725; AAC50957.1; -.
DR HSSP; O88792; 1F97.
DR Genew; HGNC:4445; GPA33.
DR MIM; 602171; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Antigen; Direct protein sequencing; Glycoprotein;
Immunoglobulin domain; Lipoprotein; Palmitate; Signal; Transmembrane.
FT SIGNAL 1 21
FT CHAIN 22 319 Cell surface A33 antigen.
FT DOMAIN 22 235 Extracellular (Potential).
FT TRANSMEM 236 256 Potential.
FT DOMAIN 257 319 Cytoplasmic (Potential).
FT DOMAIN 22 134 Ig-like V-type.
FT DOMAIN 140 227 Ig-like C2-type.
FT DOMAIN 258 261 Poly-Cys.
FT DISULFID 43 117 Potential.
FT DISULFID 146 222 Potential.
FT DISULFID 162 211 Potential.
FT CARBOHYD 112 112 N-linked (GLCNAC. . .).
FT CARBOHYD 200 200 N-linked (GLCNAC. . .) (Potential).
FT CARBOHYD 223 223 N-linked (GLCNAC. . .) (Potential).
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;

Query Match 8.4%; Score 177; DB 1; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.2e-05;
Matches 64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;
QY 4 LGLLLGLTVDYGRFILEVPESVTGPMKG-DVNLPTYPDLPQGYTVLVKM--LVQR 60
Db 8 VLMTLCAVRTVDAIS--VETPQDVLRASQGSVTLPTTYHTSTSSREGLIQWDKLLLT 64
QY 61 GSDPVTIFLRDSSGDHIQQAQYQRLHVSKV-PGDVSLQSLTLEMDDRSHYTCEVTWQT 119
Db 65 HTERVVIW-PFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVLSMS 123
QY 120 P-DGNQVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCOAR-GSPPISYIW 177
Db 124 DLEGN-----TKSRVRLVLVPPSKPECGIEGETI-IGNNIQLTQCSEKGSPTPQYSW 175
QY 178 YKQQTNNQE-----PIKVA TLSTLLFKPAVIADSGSYFCTAKGVGSE 220
Db 176 KRYNINLQEQPLAQPASGQVSLKNIST-----DTSGYIICITSSNEEGTQ 220

RESULT 8
Q66172 PRELIMINARY; PRT; 292 AA.
ID Q66172
AC Q66172;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Zgc:103642.
GN Name=zgc:103642;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Larvae;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Larvae;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081502; AAH81502.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 292 AA; 32091 MW; E1F6B5FE7A72502 CRC64;

Query Match 8.1%; Score 170.5; DB 2; Length 292;
Best Local Similarity 28.6%; Pred. No. 3.5e-05;
Matches 64; Conservative 25; Mismatches 94; Indels 41; Gaps 10;
QY 28 SVTGPMK---GDVNLPTYPDLPQGYTVLVKLVQ--RSDPVTIFLRDSSGDHIQQAQ 81
Db 22 TVTSPVKVKNEGVDLQCSYTSDFGATP-RVEMKFKDLKGSQTLVYF-----DGKPTGQ 74
QY 82 YQRLHVS HKVPGDVSLQSLTLEMDDRSHYTCEVTWQTPDGNQVRDKITELRVQKLSVS 141
Db 75 YTGRVTMY-----DKGLRFNKVTRADTGDPDCEVSGSGYGENTI-----KLTVL 119
QY 142 KPTVTGSGYGFVPOGMRISLQ-CARGSPPISYIWYKQTN-NQEPKVA TLSTLLFK 199
Db 120 VPPAKPVSRIPSSVTTSSNVRLTCFDPVGSPPSTYKWKYKNTPLPEDPTKPAFKNLTYK 179
QY 200 -----PAVT-ADSGSYFCTAKGVGSEQHSDIVKVKD 232
Db 180 MNVFNGNLFFPSVKMDTGSYFCEASNGEGVPQRGDEVKMEVRD 223

RESULT 9
Q8WMV3 PRELIMINARY; PRT; 365 AA.
ID Q8WMV3
AC Q8WMV3;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Coxsackie virus and adenovirus receptor BCAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21547769; PubMed=11688979; DOI=10.1006/bbrc.2001.5651;
RA Thoenen I., Keyaerts E., Lindberg M., Van Ranst M.,
RT "Characterization of a cDNA encoding the bovine coxsackie and
RT adenovirus receptor."
RL Biochem. Biophys. Res. Commun. 288:805-808(2001).
DR EMBL; AY033651; AAK57804.1; -.

RT	"X-ray structure of junctional adhesion molecule: structural basis for homophilic adhesion via a novel dimerization motif."
RL	EMBO J. 20:4391-4398(2001).
CC	- FUNCTION: Seems to plays a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of the PARD6-PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly. Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier.
CC	Involved in platelet activation.
CC	- SUBUNIT: Interacts with the first PDZ domain of PARD3. The association between PARD3 and PARD6B probably disrupts this interaction.
CC	- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Localized at tight junctions of both epithelial and endothelial cells.
CC	- TISSUE SPECIFICITY: Localized at tight junctions of both epithelial and endothelial cells.
CC	- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC	- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U89915; AAC32982.1; "-.
DR	PDB; 1F97; X-ray; A=27-238.
DR	MGI; MGI:1321398; F11r.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 2.
DR	SMART; SMO0406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 2.
KW	3D-structure; Glycoprotein; Immunoglobulin domain; Repeat; Signal;
KM	Tight junction; Transmembrane.
FT	SIGNAL 1 26 Potential.
FT	CHAIN 27 300 Junctional adhesion molecule 1.
FT	DOMAIN 27 238 Extracellular (Potential).
FT	TRANSMEM 239 259 Potential.
FT	DOMAIN 260 299 Cytoplasmic (Potential).
FT	DOMAIN 28 122 Ig-like V-type 1.
FT	DOMAIN 134 230 Ig-like V-type 2.
FT	DISULFID 49 108 Potential.
FT	DISULFID 152 212 Potential.
FT	CARBOHYD 42 42 N-linked (GlcNAc..)(Potential).
FT	CARBOHYD 185 185 N-linked (GlcNAc..) (Potential).
FT	STRAND 29 31
FT	STRAND 36 40
FT	TURN 41 42
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FT	STRAND 66 67
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FT	TURN 77 78
FT	STRAND 80 82
FT	HELIX 83 85
FT	TURN 86 89
FT	STRAND 90 91
FT	TURN 92 95
FT	STRAND 100 102
FT	HELIX 104 112
FT	STRAND 113 114
FT	TURN 118 129
FT	STRAND 135 137
FT	STRAND 141 143
FT	TURN 144 145

Query	Match	Best Local	Similarity	Score	DB	Length	
Matches	75;	Conservative	38;	Mismatches	127;	Indels 62; Gaps 14	
QY	3	ILIGLLGLH	LTVDTYGRPILEVPESVTGFWKGDVNL	PCTYDPLQGYTQVLVKLVQRGS	62		
Db	18	MILGSLVQ	GKGSVYT-AQSDVQVPENES-----IKLTCTY--SGFSSPRVEWKFVQGS	67			
QY	63	DPVTIFLRDSSGDHIQQA	KYQGRHVS	HKVPEGDVSLQSLTEMDRSHYTC	EVTWQTPDG	122	
Db	68	TTALVCYNSQI	-----TAPYADRVTFSSS-----GITFSSVTRKDNGETCMV---SEEG	114			
QY	123	NQVVRDKITELRVQKLSVSKPTVT	TGSGYGF	TVPQGMRI	SLQCAR-GSPPI	SIYWKQO 181	
Db	115	GQNVGEVSIHLTV-LVPPSKPTISVPS	-----SVTIGNRAVLTCSEHDSPPSEYSWFK--	167			
QY	182	TNNQEP	IKVATLST-----LLFKPAVIADSGSYFCTAKQVYSEQH	222			
Db	168	----DGISMLTADAKKTRAFNMNS	FTDPKSGDLIFDPVTA	FDPSGEYTCQAQNGYGTAMR	223		
QY	223	SDIVKFEVVKDSSKLLKTKTEAPT	MTWYPLKATSTVKQSWDWTMDG	YLGETSAG--PGK	280		
Db	224	SEAHM---	DAVELN	GVIVA	VLTLILLGLL	IPGV--WFAYS	RGYFETTKGTAPGK 277
QY	281	SL	282				
Db	278	KV	279				
RESULT 15							
Q9JHY1	PRELIMINARY;	PRT,	300	AA.			
AC	Q9JHY1;						
DT	01-OCT-2000 (Tremblrel. 15, Created)						
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)						
DT	25-OCT-2004 (Tremblrel. 28, Last annotation update)						
DE	Functional adhesion molecule JAM (functional adhesion molecule 1).						
GN	Name=Jam; Synonyms=Jam1;						
OS	Rattus norvegicus (Rat).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
OX	NCBI_TaxID=10116;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=Sprague Dawley;						
RA	Mashima H., Kojima I.;						
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Prostate;						
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;						
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,						

RA Stapleton M., Soares M.B., Bernaldo M.F., Caesavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.J., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276998; AAF78250.1; -.
DR EMBL; BC065309; AAH65309.1; -.
DR HSSP; O88792; 1F97.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; 1g; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
SQ SEQUENCE 300 AA; 32369 MW; 45AE362A96158BFA CRC64;

Query Match 8.0%; Score 167; DB 2; Length 300;
Best Local Similarity 26.3%; Pred. No. 6.8e-05;
Matches 64; Conservative 32; Mismatches 97; Indels 50; Gaps 11;

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QY      3 ILGLLLLLGHLTVDTYGRPILEVPESVTGPMWKGDVNLPTCTYDPLQGYTVLVKMLVQRG 62
Db      18 MILGSLVQCKGKSVYS-PQTAVQVPPEN-----DSVKLPCTY--SGFSSPRVEWKFVQGS 67
QY      63 DPVTIFLRDSSGDHIQQAQKYQGRLHVSHKVPFGDVSLOLSTLEMDRSHYTCEVTWQTPDG 122
Db      68 TTAIVCYNNQI-----TVPYADRVTFSSS-----GITFSSVTRKDNGEYTCMV---SEDG 114
QY      123 NQVVRDKITELRVQKLVSXSKPTVTGSGYGFVTPQGMRIQLQCAR--GSPISYIWKYKQ 181
Db      115 GQNYGEVSIHLTV-LVPPSKPTVSIPI-----SVTIGNRAVLTCSEHDSPPSEYSWFKDG 169
QY      182 TNNQEPKIVATL-----STLLFKPAVIADSGSYFCTAKGQVGSEQHSD 224
Db      170 V-----PMLTADAKKTRAFINSSYITDPKSGDVLFDVPVSAFDSGEYCEAONGYGTAMRSE 225
QY      225 IVK 227
Db      226 AVR 228

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Search completed: March 2, 2005, 15:24:31
Job time : 112 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 15:13:50 ; Search time 56 Seconds
(without alignments)
2337.317 Million cell updates/sec

Title: US-10-633-008-32

Perfect score: 2098

Sequence: 1 MGILLGLLLGLHVTVDYGR.....LDDTVPLDYEFLETKSVC 399

Scoring table: BLOSUM62

Gapop 10.0 , Gapexc 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2098	100.0	399	11	US-09-833-245-1236 Sequence 1236, Ap
2	2098	100.0	399	11	US-09-833-245-1237 Sequence 1237, Ap
3	2098	100.0	399	15	US-10-458-143-8 Sequence 8, Appli
4	2098	100.0	399	15	US-10-211-462-225 Sequence 225, Appl
5	2098	100.0	399	16	US-10-633-008-32 Sequence 32, Appl
6	2098	100.0	399	16	US-10-656-269-42 Sequence 42, Appl
7	1688	80.5	321	9	US-09-978-295A-52 Sequence 52, Appl
8	1688	80.5	321	9	US-09-978-697-52 Sequence 52, Appl
9	1688	80.5	321	9	US-09-978-192A-52 Sequence 52, Appl
10	1688	80.5	321	9	US-09-953-499-2 Sequence 2, Appli
11	1688	80.5	321	9	US-09-999-832A-52 Sequence 52, Appl
12	1688	80.5	321	10	US-09-978-189-52 Sequence 52, Appl
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853	159	7.6	352	14	US-10-219-472-216	Sequence 216, App	926	158.5	7.6	373	10	US-09-997-428-503	Sequence 503, App
854	159	7.6	352	14	US-10-219-527-216	Sequence 216, App	927	158.5	7.6	373	10	US-09-997-666-503	Sequence 503, App
855	159	7.6	352	14	US-10-227-877-216	Sequence 216, App	928	158.5	7.6	373	10	US-09-990-438-503	Sequence 503, App
856	159	7.6	352	14	US-10-223-087-280	Sequence 280, App	929	158.5	7.6	373	10	US-09-990-562-503	Sequence 503, App
857	159	7.6	352	14	US-10-223-083-280	Sequence 280, App	930	158.5	7.6	373	10	US-09-990-711-503	Sequence 503, App
858	159	7.6	352	14	US-10-216-166-216	Sequence 216, App	931	158.5	7.6	373	10	US-09-989-726-503	Sequence 503, App
859	159	7.6	352	14	US-10-218-612-216	Sequence 216, App	932	158.5	7.6	373	10	US-09-998-156-503	Sequence 503, App
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863	159	7.6	352	14	US-10-218-765-216	Sequence 216, App	936	158.5	7.6	373	10	US-09-991-157-503	Sequence 503, App
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1499	158.5	7.6	373	15	US-10-145-088A-59	Sequence 59, Appl
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ALIGNMENTS

US-09-833-245-1236
: Sequence 1236, Application US/09833245
: Publication No. US20040010134A1
: GENERAL INFORMATION:
: APPLICANT: Human Genome Sciences, Inc.
: TITLE OF INVENTION: Albumin Fusion Proteins
: FILE REFERENCE: PF546PCT
: CURRENT APPLICATION NUMBER: US/09/833, 245
: PRIOR FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: 60/229, 358
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: 60/256, 931
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/199, 384
: PRIOR FILING DATE: 2000-04-25
: NUMBER OF SEQ ID NOS: 2267
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1236
: LENGTH: 399
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-833-245-1236

Query Match	100.0%;	Score 2098;	DB 11;	Length 399;
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US-09-833-245-1237
; Sequence 1237, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1237
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1237
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; Sequence 8, Application US/10458143
; Publication No. US20040009950A1
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo D.
; TITLE OF INVENTION: SECRETED HUMAN PROTEINS
; FILE REFERENCE: 1571.003/200130.510
; CURRENT APPLICATION NUMBER: US/10/458,143
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: US/09/546,309
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
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US-10-458-143-8
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Db      301  MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGSSDEPTSQNLGNNSYDE 360
Qy      361  PCIGOEYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399
Db      361  PCIGOEYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399
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RESULT 4
US-10-211-462-225
; Sequence 225, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
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; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 225
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-225

Query Match 100.0%; Score 2098; DB 15; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.4e-179;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHGLTVDTYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
DB 1 MGILLGLLLGLHGLTVDTYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
DB 61 GSDPVTIFLRDSSGDHIQQAQKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRLSLQCCARGSPISYIWKQ 180
DB 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRLSLQCCARGSPISYIWKQ 180
QY 181 QTNNOEPIKVAATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSIDIVKFVVKDSSKLLKTK 240
DB 181 QTNNOEPIKVAATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSIDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILILISLCMVVFT 300
DB 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILILISLCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
DB 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
DB 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399

RESULT 5

US-10-633-008-32

; Sequence 32, Application US/10633008
; Publication No. US20040120957A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Van Lookren, Menno
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: USE OF A33 ANTIGENS AND JAM-IT
; FILE REFERENCE: 39766/0100P1
; CURRENT APPLICATION NUMBER: US/10/633,008
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/10/265,542
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US/09/254,465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-633-008-32

Query Match 100.0%; Score 2098; DB 16; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.4e-179;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHGLTVDTYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
DB 1 MGILLGLLLGLHGLTVDTYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
DB 61 GSDPVTIFLRDSSGDHIQQAQKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRLSLQCCARGSPISYIWKQ 180
DB 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRLSLQCCARGSPISYIWKQ 180
QY 181 QTNNOEPIKVAATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSIDIVKFVVKDSSKLLKTK 240
DB 181 QTNNOEPIKVAATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSIDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILILISLCMVVFT 300
DB 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILILISLCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
DB 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
DB 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399

RESULT 6

US-10-656-269-42

; Sequence 42, Application US/10656269
; Publication No. US20040152105A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Vogt, Lorenz
; TITLE OF INVENTION: Immune Modulatory Compounds and Methods
; FILE REFERENCE: 1700.0390002
; CURRENT APPLICATION NUMBER: US/10/656,269
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/408,233
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/449,583
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 399
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-656-269-42

Query Match 100.0%; Score 2098; DB 16; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.4e-179;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHGLTVDTYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
DB 1 MGILLGLLLGLHGLTVDTYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHTCEVTWQTP 120

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Db      61  GSDPVTIFLRDSSGDHIQQAKEYQGRLLHSHKVPGDVSLQLSTLEMDDRSHYTCBVTWQFP 120
Qy      121  DGNQVVRDKITELRVOKLSVSKPVTYTGSGYGFVPOGMRIISLQCOARGSPPISYIWKQ 180
Db      121  DGNQVVRDKITELRVOKLSVSKPVTYTGSGYGFVPOGMRIISLQCOARGSPPISYIWKQ 180
Qy      181  QTNNGEPIKVATLSTLLFKPAVIADSGSYFCTAKQVGSSEQHSPIVKFVKDSSKLTXTK 240
Db      181  QTNNGEPIKVATLSTLLFKPAVIADSGSYFCTAKQVGSSEQHSPIVKFVKDSSKLTXTK 240
Qy      241  TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
Db      241  TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
Qy      301  MAYIMLCRKTSQOEHVYEAPARAHAREANDSGETMRVAIFASGCSDEPTSONLGNNYSDE 360
Db      301  MAYIMLCRKTSQOEHVYEAPARAHAREANDSGETMRVAIFASGCSDEPTSONLGNNYSDE 360
Qy      361  PCIGQEVQIIAQINGNYARLLDTVPLDYEFPLATEGKSVK 399
Db      361  PCIGQEVQIIAQINGNYARLLDTVPLDYEFPLATEGKSVK 399
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RESULT 7

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US-09-978-295A-52
; Sequence 52, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR FILING DATE: 1998-04-09
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; PRIOR FILING DATE: 1998-04-15
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;; PRIOR FILING DATE: 1998-04-15
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;; PRIOR APPLICATION NUMBER: 60/082704
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15

;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 80.5%; Score 1688; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDNLPCTYDPLQGYTVLVKLVQR 60

Db 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDNLPCTYDPLQGYTVLVKLVQR 60

QY 61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHKVPGBVSLQLSTLEMDDRSHYTCETWQTP 120

Db 61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHKVPGBVSLQLSTLEMDDRSHYTCETWQTP 120

QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRLISLQCCQARGSPISYTWYKQ 180

Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVTPQGMRLISLQCCQARGSPISYTWYKQ 180

QY 181 QTNQPEPIKVAATLSTLFRPAVIADSGSYFCTAKQVGSSEQHSDIVKFPVVKDSKLLKTK 240

Db 181 QTNQPEPIKVAATLSTLFRPAVIADSGSYFCTAKQVGSSEQHSDIVKFPVVKDSKLLKTK 240

QY 241 TEAPTTMTYPLKATSTVQSWDWTMDGYLGETSAGPKSLPVFAIILISLCMVVFT 300

Db 241 TEAPTTMTYPLKATSTVQSWDWTMDGYLGETSAGPKSLPVFAIILISLCMVVFT 300

QY 301 MAYIMLCRKTSQOEHYVEAAR 321

Db 301 MAYIMLCRKTSQOEHYVEAAR 321

RESULT 8

US-09-978-697-52

; Sequence 52, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerltsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kijavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC27
;; CURRENT APPLICATION NUMBER: US/09/978, 697

1	CURRENT FILING DATE: 2001-10-16
2	PRIOR APPLICATION NUMBER: 09/918585
3	PRIOR FILING DATE: 2001-07-30
4	PRIOR APPLICATION NUMBER: 60/062250
5	PRIOR FILING DATE: 1997-10-17
6	PRIOR APPLICATION NUMBER: 60/064249
7	PRIOR FILING DATE: 1997-11-03
8	PRIOR APPLICATION NUMBER: 60/065311
9	PRIOR FILING DATE: 1997-11-13
10	PRIOR APPLICATION NUMBER: 60/066364
11	PRIOR FILING DATE: 1997-11-21
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21	PRIOR FILING DATE: 1998-03-12
22	PRIOR APPLICATION NUMBER: 60/078004
23	PRIOR FILING DATE: 1998-03-13
24	PRIOR APPLICATION NUMBER: 60/078886
25	PRIOR FILING DATE: 1998-03-20
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29	PRIOR FILING DATE: 1998-03-20
30	PRIOR APPLICATION NUMBER: 60/078939
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32	PRIOR APPLICATION NUMBER: 60/079294
33	PRIOR FILING DATE: 1998-03-25
34	PRIOR APPLICATION NUMBER: 60/079656
35	PRIOR FILING DATE: 1998-03-26
36	PRIOR APPLICATION NUMBER: 60/079664
37	PRIOR FILING DATE: 1998-03-27
38	PRIOR APPLICATION NUMBER: 60/079689
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73	PRIOR FILING DATE: 1998-04-08

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1 80.5%; Score 1688; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 DGNQVVRDKITELRVQKLSVSKPIVTTGSGYGFTVPQGMRLSLQCCARGSPISYIWKQ 180
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QY 181 QTNNOEPKIVATLSTLFFKPAVIADSGSYFCTAKQVGSSEQHSDIVKFVVKDSSKLLKTK 240
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QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVFT 300
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QY 301 MAYIMLCRKTSQOEHVYEAAAR 321
Db 301 MAYIMLCRKTSQOEHVYEAAAR 321

RESULT 9
US-09-978-192A-52
; Sequence 52, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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QY 241 TEAPTTMTYPLKATSTVQSWDWTMDMGYLGETSAGPGKSLPVFAIILITISLCCMVFT 300
Db 241 TEAPTTMTYPLKATSTVQSWDWTMDMGYLGETSAGPGKSLPVFAIILITISLCCMVFT 300
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Db 301 MAYIMLCRKTSQOEHYEAR 321

RESULT 10
US-09-953-499-2
; Sequence 2, Application US/09953499
; Publication No. US20020182206A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.


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; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/953, 499
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/254, 465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066, 364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078, 936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-2
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Query Match 80.5%; Score 1688; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRILVSHKVPBGDVSLOISTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLSLQCCARGSPPISTWYKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLSLQCCARGSPPISTWYKQ 180
QY 181 QTNNGEPIKAVATLSTLLFKPAVIADSGSYFCTAKQGVSEGHSDIVKVVKDSKSLKTK 240
Db 181 QTNNGEPIKAVATLSTLLFKPAVIADSGSYFCTAKQGVSEGHSDIVKVVKDSKSLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWMTTMDGYLGETSAGPGKSLPVFAIILISLCMVFT 300
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QY 301 MAYIMLCRKTSQOEHVYEAAR 321
Db 301 MAYIMLCRKTSQOEHVYEAAR 321
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RESULT 11
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James'
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
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; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 80.5%; Score 1688; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLTLVTDTYGRPILEVPESVTGPMKGVNLPTTYDPLQGYTVLVKLVQR 60
Db 1 MGILLGLLLGLTLVTDTYGRPILEVPESVTGPMKGVNLPTTYDPLQGYTVLVKLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLOLSTLEMDDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLOLSTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFYVQGMKRISLQCCQARGSPPISTIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFYVQGMKRISLQCCQARGSPPISTIWKQ 180
QY 181 QTNNOPIKVAATLSTLFPKPAVIADSGSYFCTAKGVGSEQHSDIVKFPVVKDSSKLLKTK 240
Db 181 QTNNOPIKVAATLSTLFPKPAVIADSGSYFCTAKGVGSEQHSDIVKFPVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTYKQSWDWTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 300
Db 241 TEAPTTMTYPLKATSTYKQSWDWTMDGYLGSTAGPGKSLPVFAILLISLCMVFT 300
QY 301 MAYIMLCRKTSQOEHYVEAAR 321
Db 301 MAYIMLCRKTSQOEHYVEAAR 321

RESULT 12
US-09-978-189-52
; Sequence 52, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paonl, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-03-10
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 80.5%; Score 1688; DB 10; Length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLLTVDTYGRPILEVPEPVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHLLTVDTYGRPILEVPEPVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLISLQCCQARGSPPIISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLISLQCCQARGSPPIISYIWKQ 180
QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFFVVKDSSKLLKTK 240
Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLIISLCMVVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLIISLCMVVFT 300

Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLIISLCMVVFT 300
QY 301 MAYIMLCRKTSQOEHYVEAR 321
Db 301 MAYIMLCRKTSQOEHYVEAR 321

RESULT 13
US-09-978-608A-52
; Sequence 52, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 52
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-52

Query Match 80.5%; Score 1688; DB 10; Length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHLLTVDTYGRPILEVPEPVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHLLTVDTYGRPILEVPEPVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLISLQCCQARGSPPIISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRLISLQCCQARGSPPIISYIWKQ 180
QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFFVVKDSSKLLKTK 240
Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLIISLCMVVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLIISLCMVVFT 300

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Db      241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLISLCMVFT 300
QY      301 MAYIMLCRKTSQOEHVYEAAAR 321
Db      301 MAYIMLCRKTSQOEHVYEAAAR 321
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RESULT 14

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US-09-978-585A-52
; Sequence 52, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnayers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 52
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-52
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Query Match      80.5%; Score 1688; DB 10; length 321;
Best Local Similarity 100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MGILLGLLLGLHLYVDYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTOVLVKMLVQR 60
Db      1 MGILLGLLLGLHLYVDYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTOVLVKMLVQR 60

QY      61 GSDPVTIFLRDSSGDHIQQAQKQGRHLVSHKVPBGDVSLSQLSTLEMDDRSHYTCCEVTMOTP 120
Db      61 GSDPVTIFLRDSSGDHIQQAQKQGRHLVSHKVPBGDVSLSQLSTLEMDDRSHYTCCEVTMOTP 120

QY      121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFVPGQMRISLQCCQARGSPPISTYMWKQ 180
Db      121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFVPGQMRISLQCCQARGSPPISTYMWKQ 180

QY      181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVSGEHSDIVKPVVKDSSKLTK 240
Db      181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVSGEHSDIVKPVVKDSSKLTK 240
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QY      241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLISLCMVFT 300
Db      241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAILLISLCMVFT 300
QY      301 MAYIMLCRKTSQOEHVYEAAAR 321
Db      301 MAYIMLCRKTSQOEHVYEAAAR 321
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RESULT 15

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US-09-978-191A-52
; Sequence 52, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnayers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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OM protein - protein search, using sw model

Run on: March 2, 2005, 15:20:52 ; Search time 489 Seconds
(without alignments)
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Perfect score: 2098
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	2098	100.0	399	1 PCT-US01-11988-1237	Sequence 1237, Ap
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6	2098	100.0	399	1 PCT-US02-08123-1434	Sequence 1434, Ap
7	2098	100.0	399	1 PCT-US02-08124-592	Sequence 592, App
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119	1688	80.5	321	27	US-10-145-089A-52	Sequence 52, Appl	192	840	40.0	280	32	US-10-656-269-14	Sequence 14, Appl
120	1688	80.5	321	27	US-10-145-092A-52	Sequence 52, Appl	193	840	40.0	280	35	US-10-964-263-8	Sequence 8, Appli
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122	1688	80.5	321	27	US-10-145-124A-52	Sequence 52, Appl	195	738	35.2	143	21	US-09-724-676A-67203	Sequence 67203, A
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124	1688	80.5	321	27	US-10-145-129A-52	Sequence 52, Appl	197	654	31.2	147	21	US-09-724-676A-67204	Sequence 67204, A
125	1688	80.5	321	27	US-10-152-388B-52	Sequence 52, Appl	198	653	31.1	131	21	US-09-724-676-67205	Sequence 67205, A
126	1688	80.5	321	27	US-10-160-502A-52	Sequence 52, Appl	199	653	30.9	131	21	US-09-724-676A-67205	Sequence 67205, A
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128	1688	80.5	321	27	US-10-162-522A-52	Sequence 52, Appl	201	647.5	30.9	208	21	US-09-724-676A-67200	Sequence 67200, A
129	1688	80.5	321	27	US-10-164-728A-52	Sequence 52, Appl	202	624.5	29.8	139	27	US-10-170-205E-22636	Sequence 22636, A
130	1688	80.5	321	27	US-10-164-749-52	Sequence 52, Appl	203	624.5	29.8	139	37	US-60-452-680-16137	Sequence 16137, A
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137	1688	80.5	321	27	US-10-165-353A-52	Sequence 52, Appl	210	178.5	8.5	296	37	US-60-453-050-11599	Sequence 11599, A
138	1688	80.5	321	27	US-10-166-709A-52	Sequence 52, Appl	211	178.5	8.5	296	37	US-60-453-135-11599	Sequence 11599, A
139	1688	80.5	321	27	US-10-167-600-52	Sequence 52, Appl	212	178.5	8.5	296	37	US-60-455-444-6070	Sequence 6070, Ap
140	1688	80.5	321	27	US-10-167-600A-52	Sequence 52, Appl	213	178.5	8.5	296	37	US-60-465-241-6070	Sequence 6070, Ap
141	1688	80.5	321	27	US-10-167-719A-52	Sequence 52, Appl	214	178.5	8.5	296	37	US-60-466-412-11599	Sequence 11599, A
142	1688	80.5	321	27	US-10-167-719A-52	Sequence 52, Appl	215	178.5	8.5	296	37	US-60-466-412-11599	Sequence 11599, A

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ALIGNMENTS

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RESULT 1
PCT-US00-31162A-63
; Sequence 63, Application PC/TUS0031162A
; GENERAL INFORMATION:
;   APPLICANT: Human Genome Sciences, Inc.
;   TITLE OF INVENTION: 18 Human Secreted Proteins
;   FILE REFERENCE: PS717PCT
;   CURRENT APPLICATION NUMBER: PCT/US00/31162A
;   CURRENT FILING DATE: 2000-11-15
;   PRIOR APPLICATION NUMBER: 60/166,415
;   PRIOR FILING DATE: 1999-11-19
;   PRIOR APPLICATION NUMBER: 60/215,136
;   NUMBER OF SEQ ID NOS: 161
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 63
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US00-31162A-63

Query Match          100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
PCT-US00-31162A-85
; Sequence 85, Application PC/TUS0031162A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 18 Human Secreted Proteins
; FILE REFERENCE: PS717PCT
; CURRENT APPLICATION NUMBER: PCT/US00/31162A
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/166,415
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/215,136
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-31162A-85

Query Match 100.0%; Score 2098; DB 1; Length 399;
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RESULT 3
PCT-US01-11988-1236
; Sequence 1236, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229,358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256,931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199,384
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1236
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-1236

Query Match 100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4
PCT-US01-11988-1237
; Sequence 1237, Application PC/TUS0111988
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins

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; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
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; PRIOR FILING DATE: 2000-12-21
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; PRIOR FILING DATE: 2000-04-25
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; PCT-US01-11988-1237
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Db 181 QTNNOEPKIVATLSTLLFKPAVIADSGSYFCTAKGVSEQHSDIVKFWKDSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPVFAILLISLCCMVVFT 300
   |||||||
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPVFAILLISLCCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
   |||||||
Db 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNYARLLDTPVPLDYEFPLATEGKSVC 399
   |||||||
Db 361 PCIGOEYQIIAQINGNYARLLDTPVPLDYEFPLATEGKSVC 399
```

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RESULT 5
PCT-US02-04915-225
; Sequence 225, Application PC/TUS0204915
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200PC
; CURRENT APPLICATION NUMBER: PCT/US02/04915
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/285,475
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/350,666
```

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; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 225
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-04915-225
```

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Query Match          100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGILLGLLLGLHGLTVDTYGRPILEVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
   |||||||
Db 1 MGILLGLLLGLHGLTVDTYGRPILEVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120
   |||||||
Db 61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVRDKITELRVOKLSVSKPTVTGSGYGFVTPQGMRLSLQCCARGSPISYIWKQ 180
   |||||||
Db 121 DGNQVRDKITELRVOKLSVSKPTVTGSGYGFVTPQGMRLSLQCCARGSPISYIWKQ 180
QY 181 QTNNOEPKIVATLSTLLFKPAVIADSGSYFCTAKGVSEQHSDIVKFWKDSKLLKTK 240
   |||||||
Db 181 QTNNOEPKIVATLSTLLFKPAVIADSGSYFCTAKGVSEQHSDIVKFWKDSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPVFAILLISLCCMVVFT 300
   |||||||
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPVFAILLISLCCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
   |||||||
Db 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNYARLLDTPVPLDYEFPLATEGKSVC 399
   |||||||
Db 361 PCIGOEYQIIAQINGNYARLLDTPVPLDYEFPLATEGKSVC 399
```

```

RESULT 6
PCT-US02-08123-1434
; Sequence 1434, Application PC/TUS0208123
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS904PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08123
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 2048
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1434
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-08123-1434
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```

Query Match          100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MGILLGLLLGLHGLTVDTYGRPILEVESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
   |||||||
```


Db 1 MGILLGLLLGLH LTVDTYGRPILEVPE SVTGPMKGDVNL PCTYDPLQGYTQVLVKMLVQR 60

QY 61 GSDPVTIFLRDSSGDHIQQA KYQGR LHVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120

Db 61 GSDPVTIFLRDSSGDHIQQA KYQGR LHVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120

QY 121 DGNQVVRDKITELRVOKLSVSKPTVTGSGYGF TVPQGMRI SLQCCQARGSPPI SYIWKQ 180

Db 121 DGNQVVRDKITELRVOKLSVSKPTVTGSGYGF TVPQGMRI SLQCCQARGSPPI SYIWKQ 180

QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVGS EQHSDIVKFVVKDSSKLLKTK 240

Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVGS EQHSDIVKFVVKDSSKLLKTK 240

QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLG ETSAGPGKSLPVFAIILISLCCMVVFT 300

Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLG ETSAGPGKSLPVFAIILISLCCMVVFT 300

QY 301 MAYIMLCRKTSQQE HVEAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360

Db 301 MAYIMLCRKTSQQE HVEAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360

QY 361 PCIGQEQYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399

Db 361 PCIGQEQYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399

RESULT 7

PCT-US02-08124-592

; Sequence 592, Application PC/TUS0208124

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS901PCT

; CURRENT APPLICATION NUMBER: PCT/US02/08124

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: US 60/331,287

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/306,171

; PRIOR FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: US 60/277,340

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 857

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 592

; LENGTH: 399

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US02-08124-592

Query Match 100.0%; Score 2098; DB 1; Length 399;

Best Local Similarity 100.0%; Pred. No. 2.6e-193;

Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLH LTVDTYGRPILEVPE SVTGPMKGDVNL PCTYDPLQGYTQVLVKMLVQR 60

Db 1 MGILLGLLLGLH LTVDTYGRPILEVPE SVTGPMKGDVNL PCTYDPLQGYTQVLVKMLVQR 60

QY 61 GSDPVTIFLRDSSGDHIQQA KYQGR LHVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120

Db 61 GSDPVTIFLRDSSGDHIQQA KYQGR LHVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120

QY 121 DGNQVVRDKITELRVOKLSVSKPTVTGSGYGF TVPQGMRI SLQCCQARGSPPI SYIWKQ 180

Db 121 DGNQVVRDKITELRVOKLSVSKPTVTGSGYGF TVPQGMRI SLQCCQARGSPPI SYIWKQ 180

QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVGS EQHSDIVKFVVKDSSKLLKTK 240

Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVGS EQHSDIVKFVVKDSSKLLKTK 240

QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLG ETSAGPGKSLPVFAIILISLCCMVVFT 300

Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLG ETSAGPGKSLPVFAIILISLCCMVVFT 300

QY 301 MAYIMLCRKTSQQE HVEAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360

Db 301 MAYIMLCRKTSQQE HVEAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360

QY 361 PCIGQEQYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399

Db 361 PCIGQEQYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399

RESULT 8

PCT-US02-08276-446

; Sequence 446, Application PC/TUS0208276

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS906PCT

; CURRENT APPLICATION NUMBER: PCT/US02/08276

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: US 60/331,287

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/306,171

; PRIOR FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: US 60/277,340

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 650

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 446

; LENGTH: 399

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US02-08276-446

Query Match 100.0%; Score 2098; DB 1; Length 399;

Best Local Similarity 100.0%; Pred. No. 2.6e-193;

Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLH LTVDTYGRPILEVPE SVTGPMKGDVNL PCTYDPLQGYTQVLVKMLVQR 60

Db 1 MGILLGLLLGLH LTVDTYGRPILEVPE SVTGPMKGDVNL PCTYDPLQGYTQVLVKMLVQR 60

QY 61 GSDPVTIFLRDSSGDHIQQA KYQGR LHVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120

Db 61 GSDPVTIFLRDSSGDHIQQA KYQGR LHVSHKVPGDVSLQSLTLEMDDRSHYTCEVTWQTP 120

QY 121 DGNQVVRDKITELRVOKLSVSKPTVTGSGYGF TVPQGMRI SLQCCQARGSPPI SYIWKQ 180

Db 121 DGNQVVRDKITELRVOKLSVSKPTVTGSGYGF TVPQGMRI SLQCCQARGSPPI SYIWKQ 180

QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVGS EQHSDIVKFVVKDSSKLLKTK 240

Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGQVGS EQHSDIVKFVVKDSSKLLKTK 240

QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLG ETSAGPGKSLPVFAIILISLCCMVVFT 300

Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLG ETSAGPGKSLPVFAIILISLCCMVVFT 300

QY 301 MAYIMLCRKTSQQE HVEAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360

Db 301 MAYIMLCRKTSQQE HVEAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360

QY 361 PCIGQEQYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399

Db 361 PCIGQEQYQIIAQINGNYARLLDTPVPLDYEFLATEGKSVC 399

RESULT 9

PCT-US02-08277-931

; Sequence 931, Application PC/TUS0208277

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS907PCT

; CURRENT APPLICATION NUMBER: PCT/US02/08277
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 1357
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 931
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08277-931

Query Match 100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQOAKYQGRHLVSHKVPGDVSLQSTLEMDDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQOAKYQGRHLVSHKVPGDVSLQSTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLISLQCCARGSPPISTYWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLISLQCCARGSPPISTYWKQ 180
QY 181 QTNNOEPRIKAVATLSTLFFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
Db 181 QTNNOEPRIKAVATLSTLFFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAAREANDSGETMRVAIFASGCSSDEPTSONLGNNYSDE 360
Db 301 MAYIMLCRKTSQOEHVYEAAARAHAAREANDSGETMRVAIFASGCSSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNVARLLDTPVPLDYEFLATEGKSVC 399
Db 361 PCIGOEYQIIAQINGNVARLLDTPVPLDYEFLATEGKSVC 399

RESULT 10
PCT-US02-08278-1373
; Sequence 1373, Application PC/TUS0208278
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS902PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08278
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; NUMBER OF SEQ ID NOS: 1988
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1373
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-08278-1373
Query Match 100.0%; Score 2098; DB 1; Length 399;

Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQOAKYQGRHLVSHKVPGDVSLQSTLEMDDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQOAKYQGRHLVSHKVPGDVSLQSTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLISLQCCARGSPPISTYWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLISLQCCARGSPPISTYWKQ 180
QY 181 QTNNOEPRIKAVATLSTLFFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
Db 181 QTNNOEPRIKAVATLSTLFFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAAREANDSGETMRVAIFASGCSSDEPTSONLGNNYSDE 360
Db 301 MAYIMLCRKTSQOEHVYEAAARAHAAREANDSGETMRVAIFASGCSSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNVARLLDTPVPLDYEFLATEGKSVC 399
Db 361 PCIGOEYQIIAQINGNVARLLDTPVPLDYEFLATEGKSVC 399

RESULT 11
PCT-US02-09785-795
; Sequence 795, Application PC/TUS0209785
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS905PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09785
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 795
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09785-795
Query Match 100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHGLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQOAKYQGRHLVSHKVPGDVSLQSTLEMDDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQOAKYQGRHLVSHKVPGDVSLQSTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLISLQCCARGSPPISTYWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLISLQCCARGSPPISTYWKQ 180
QY 181 QTNNOEPRIKAVATLSTLFFKPAVIADSGSYFCTAKGVGSEQHSDIVKFVVKDSSKLLKTK 240

Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
Db 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNYARLLDTVPPLDYEFLLATEGKSVC 399
Db 361 PCIGOEYQIIAQINGNYARLLDTVPPLDYEFLLATEGKSVC 399

RESULT 12
PCT-US03-31207-32
; Sequence 32, Application PC/TUS0331207
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Guiney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tupmas, Daniel
; APPLICANT: Vap Lookren, Menno
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Use of A33 Antigens and Jam-It
; FILE REFERENCE: 39766-0100PCT
; CURRENT APPLICATION NUMBER: PCT/US03/31207
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 10/633,008
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 10/265,542
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-31207-32

Query Match 100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGILLGLLLGLHTVDYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHTVDYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQSLSTLEMDDRSHTYCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQSLSTLEMDDRSHTYCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCCQARGSPPIISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCCQARGSPPIISYIWKQ 180
QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFVVKDSSKLLKTK 240
Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFVVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILISLCCMVVFT 300
QY 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
Db 301 MAYIMLCRKTSQOEHVYEAAARAHAREANDSGETMRVAIFASGCCSDEPTSONLGNNYSDE 360
QY 361 PCIGOEYQIIAQINGNYARLLDTVPPLDYEFLLATEGKSVC 399

Db 361 PCIGOEYQIIAQINGNYARLLDTVPPLDYEFLLATEGKSVC 399

RESULT 13
PCT-US04-34163-319
; Sequence 319, Application PC/TUS0434163
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Pauloski, Nicole
; APPLICANT: Taylor, Ian
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: GENE EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 5176
; CURRENT APPLICATION NUMBER: PCT/US04/34163
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/508,355
; PRIOR FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 400
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 319
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-34163-319

Query Match 100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGILLGLLLGLHTVDYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHTVDYGRPILEVPEESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQSLSTLEMDDRSHTYCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPGDVSLQSLSTLEMDDRSHTYCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCCQARGSPPIISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRISLQCCQARGSPPIISYIWKQ 180
QY 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFVVKDSSKLLKTK 240
Db 181 QTNNOEPIKAVATLSTLLFKPAVIADSGSYFCTAKGVGSEQHSIDIVKFVVKDSSKLLKTK 240
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RESULT 14
US-09-546-309-8
; Sequence 8, Application US/09546309
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo D.
; TITLE OF INVENTION: SECRETED HUMAN PROTEINS
; FILE REFERENCE: 1571.003/200130.510
; CURRENT APPLICATION NUMBER: US/09/546,309
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 399
; TYPE: PRT

ORGANISM: Homo sapiens
US-09-546-309-8

US-09-546-309-8

Query Match	100.0%;	Score 2098;	DB 19;	Length 399;
Best Local Similarity	100.0%;	Pred. No. 2.6e-193;		
Matches 399;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY	241	TEAPTMT	YPLKAT	STVKQ	SWMTT	MDGYL	GETS	SAGP	KSPL	PVFAI	ILISLCMVFT	300
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QY	301	MAYIMLC	RKTSQ	QEHV	EAARAH	AREAND	SGET	MRVAI	FASG	CS	SDEPTSQNLGNYSDE	360
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RESULT 15

US-09-833-245-1236

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: Sequence 1236, Application US/09833245
: GENERAL INFORMATION:
: APPLICANT: Human Genome Sciences, Inc.
: TITLE OF INVENTION: Albumin Fusion Proteins
: FILE REFERENCE: PE546PCT
: CURRENT APPLICATION NUMBER: US/09/833,245
: CURRENT FILING DATE: 2001-04-12
: PRIOR APPLICATION NUMBER: 60/229, 358
: PRIOR FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: 60/256, 931
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/199, 384
: PRIOR FILING DATE: 2000-04-25
: NUMBER OF SEQ ID NOS: 2267
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1236:
: LENGTH: 399
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-833-245-1236

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Best Local Similarity	100.0%;	Pred. No. 2.6e-193;		
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 15:16:16 ; Search time 26 Seconds
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Searched: 181127 seqs, 44957854 residues

Total number of hits satisfying chosen parameters: 181127

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	870	41.5	175	6	US-10-986-822-6 Sequence 6, Appl
3	178.5	8.5	335	6	US-10-523-834-330 Sequence 330, App
4	159	7.6	365	6	US-10-155-282B-11 Sequence 11, Appl
5	159	7.6	365	8	US-60-651-509-101 Sequence 101, App
6	159	7.6	365	8	US-60-651-509-103 Sequence 103, App
7	158.5	7.5	373	5	US-09-978-191C-59 Sequence 59, Appl
8	157.5	7.5	351	6	US-10-523-834-331 Sequence 331, App
9	156	7.4	737	6	US-10-450-763-32378 Sequence 32378, A
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11	153.5	7.3	5518	7	US-11-049-637-2 Sequence 2, Appl
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13	146.5	7.0	361	6	US-10-450-763-52760 Sequence 52760, A
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15	139	6.6	545	1	PCT-US05-02350-272 Sequence 272, App
16	139	6.6	545	7	US-11-043-770-272 Sequence 272, App
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111	108	5.1	628	7	US-11-043-591-103	Sequence 103, App
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115	107	5.1	732	7	US-11-038-956-5	Sequence 5, Appli
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181	99.5	4.7	248	7	US-11-054-515-1657	Sequence 1657, App
182	99.5	4.7	248	7	US-11-054-515-1660	Sequence 1660, App
183	99.5	4.7	248	7	US-11-054-515-1670	Sequence 1670, App
184	99.5	4.7	1021	7	US-11-033-545-363	Sequence 363, App
185	99.5	4.7	1685	6	US-10-450-763-42696	Sequence 42696, A
186	99	4.7	237	6	US-10-450-763-49659	Sequence 49659, A
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188	98.5	4.7	248	7	US-11-054-515-1417	Sequence 1417, App
189	98.5	4.7	421	7	US-11-051-724-96	Sequence 96, Appl
190	98.5	4.7	421	7	US-11-051-724-98	Sequence 98, Appl
191	98.5	4.7	482	1	PCT-IB03-06509-3961	Sequence 3961, App
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193	98.5	4.7	917	7	US-11-056-730-18	Sequence 18, Appl
194	98.5	4.7	917	7	US-11-056-730-20	Sequence 20, Appl
195	98.5	4.7	1225	6	US-10-450-763-34308	Sequence 34308, A
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197	98	4.7	600	6	US-10-184-644-586	Sequence 586, App
198	97.5	4.6	244	7	US-11-054-515-1524	Sequence 1524, App
199	97.5	4.6	248	7	US-11-054-515-1623	Sequence 1623, App
200	97.5	4.6	759	7	US-11-043-591-123	Sequence 123, App
201	97.5	4.6	838	7	US-11-043-591-462	Sequence 462, App
202	97.5	4.6	982	6	US-10-450-763-41910	Sequence 41910, A
203	97.5	4.6	1023	6	US-10-450-763-59027	Sequence 59027, A
204	97	4.6	255	7	US-11-054-515-1483	Sequence 1483, App
205	97	4.6	388	8	US-60-651-509-703	Sequence 703, App
206	97	4.6	388	8	US-60-651-509-704	Sequence 704, App
207	97	4.6	739	1	PCT-US04-31825-3	Sequence 3, Appli
208	97	4.6	1483	6	US-10-450-763-46695	Sequence 46695, A
209	96.5	4.6	225	7	US-11-021-951-158	Sequence 158, App
210	96.5	4.6	245	7	US-11-054-515-1860	Sequence 1860, App
211	96.5	4.6	248	7	US-11-054-515-965	Sequence 965, App
212	96.5	4.6	248	7	US-11-054-515-980	Sequence 980, App
213	96.5	4.6	1573	1	PCT-US03-41242-63	Sequence 63, Appl
214	96	4.6	244	6	US-10-450-763-49648	Sequence 49648, A
215	96	4.6	365	6	US-10-450-763-53217	Sequence 53217, A
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218	95.5	4.6	248	7	US-11-054-515-1755	Sequence 1755, App
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220	95.5	4.6	251	7	US-11-054-515-1207	Sequence 1207, App
221	95.5	4.6	252	7	US-11-054-515-1462	Sequence 1462, App
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224	95.5	4.6	917	7	US-11-056-730-26	Sequence 26, Appl
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230	94.5	4.5	194	7	US-11-043-591-110	Sequence 110, App
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236	94.5	4.5	248	7	US-11-054-515-1681	Sequence 1681, App
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238	94.5	4.5	277	6	US-10-450-763-50119	Sequence 50119, A
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240	94.5	4.5	999	6	US-10-184-644-434	Sequence 434, App
241	94.5	4.5	1888	6	US-10-450-763-53573	Sequence 53573, A
242	94	4.5	236	6	US-10-450-763-49652	Sequence 49652, A
243	94	4.5	243	6	US-11-054-515-1533	Sequence 1533, App
244	94	4.5	1359	6	US-10-450-763-39944	Sequence 39944, A

245	94	4.5	9222	6	US-10-450-763-51423	Sequence 51423, A
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247	93.5	4.5	244	7	US-11-054-515-1214	Sequence 1214, Ap
248	93.5	4.5	248	7	US-11-054-515-1643	Sequence 1643, Ap
249	93.5	4.5	458	7	US-11-039-144-2	Sequence 2, Appl1
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254	93	4.4	249	7	US-11-054-515-1620	Sequence 1620, Ap
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259	92.5	4.4	245	1	PCT-US04-42360-291	Sequence 291, App
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262	92.5	4.4	248	7	US-11-054-515-953	Sequence 953, App
263	92.5	4.4	250	7	US-11-054-515-2074	Sequence 2074, App
264	92.5	4.4	282	6	US-10-184-644-218	Sequence 218, App
265	92.5	4.4	282	7	US-11-050-926-348	Sequence 348, App
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272	92.5	4.4	764	8	US-60-651-509-467	Sequence 467, App
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276	92.5	4.4	902	7	US-11-056-730-14	Sequence 14, Appl1
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282	92	4.4	583	7	US-11-051-454-12	Sequence 12, Appl1
283	92	4.4	583	8	US-60-651-509-418	Sequence 418, App
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286	91.5	4.4	252	7	US-11-054-515-1713	Sequence 1713, Ap
287	91.5	4.4	433	7	US-11-021-951-129	Sequence 129, App
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292	91	4.3	250	7	US-11-054-515-1867	Sequence 1867, App
293	91	4.3	398	8	US-60-651-509-522	Sequence 522, App
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295	91	4.3	438	6	US-10-450-763-45185	Sequence 45185, A
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297	90.5	4.3	224	7	US-11-043-591-111	Sequence 111, App
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299	90.5	4.3	244	7	US-11-054-515-1507	Sequence 1507, App
300	90.5	4.3	248	7	US-11-054-515-1386	Sequence 1386, App
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302	90.5	4.3	250	7	US-11-054-515-859	Sequence 859, App
303	90.5	4.3	251	7	US-11-054-515-1383	Sequence 1383, App
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306	90.5	4.3	251	7	US-11-054-515-1800	Sequence 1800, App
307	90.5	4.3	260	7	US-11-054-515-1244	Sequence 1244, App
308	90.5	4.3	473	8	US-60-651-509-378	Sequence 378, App1
309	90.5	4.3	479	1	PCT-US04-43806-33	Sequence 33, Appl1
310	90.5	4.3	479	7	US-11-024-251-33	Sequence 33, Appl1
311	90.5	4.3	733	6	US-10-450-763-58502	Sequence 58502, A
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315	90	4.3	251	7	US-11-054-515-852	Sequence 852, App
316	90	4.3	251	7	US-11-054-515-1074	Sequence 1074, App
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318	90	4.3	318	7	US-11-054-515-1590	Sequence 1590, App1
319	90	4.3	319	1	PCT-US04-38197-59	Sequence 59, Appl1
320	90	4.3	320	7	US-11-033-545-454	Sequence 454, App
321	89.5	4.3	321	6	US-10-450-763-36692	Sequence 36692, A
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323	89.5	4.3	323	7	US-11-054-515-845	Sequence 845, App
324	89.5	4.3	324	7	US-11-054-515-853	Sequence 853, App
325	89.5	4.3	325	7	US-11-054-515-940	Sequence 940, App
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338	89	4.2	338	7	US-11-054-515-1965	Sequence 1965, App
339	89	4.2	339	7	US-11-054-515-1974	Sequence 1974, App
340	89	4.2	340	7	US-11-054-515-1631	Sequence 1631, App
341	89	4.2	341	6	US-10-450-763-50295	Sequence 50295, A
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343	89	4.2	343	8	US-60-651-509-524	Sequence 524, App
344	89	4.2	344	8	US-60-651-509-525	Sequence 525, App
345	89	4.2	345	6	US-10-450-763-46426	Sequence 46426, A
346	89	4.2	346	6	US-10-450-763-48872	Sequence 48872, A
347	89	4.2	347	6	US-10-938-061-136	Sequence 136, App
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349	89	4.2	349	6	US-11-051-724-90	Sequence 90, Appl1
350	88.5	4.2	350	6	US-10-450-763-52697	Sequence 52697, A
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352	88.5	4.2	352	7	US-11-054-515-1369	Sequence 1369, App
353	88.5	4.2	353	7	US-11-054-515-1764	Sequence 1764, App
354	88.5	4.2	354	7	US-11-054-515-2072	Sequence 2072, App
355	88.5	4.2	355	7	US-11-054-515-1388	Sequence 1388, App
356	88.5	4.2	356	7	US-11-054-515-1529	Sequence 1529, App
357	88.5	4.2	357	7	US-11-054-515-944	Sequence 944, App
358	88.5	4.2	358	7	US-11-054-515-1062	Sequence 1062, App
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361	88.5	4.2	361	7	US-11-054-515-1297	Sequence 1297, App
362	88.5	4.2	362	7	US-11-054-515-1253	Sequence 1253, App
363	88.5	4.2	363	1	PCT-US04-38197-36	Sequence 36, Appl1
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366	88.5	4.2	366	7	US-11-033-545-448	Sequence 448, App
367	88.5	4.2	367	7	US-11-033-545-321	Sequence 321, App
368	88.5	4.2	368	6	US-10-450-763-35137	Sequence 35137, A
369	88	4.2	369	8	US-60-651-509-270	Sequence 270, App
370	88	4.2	370	8	US-60-651-509-271	Sequence 271, App
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372	88	4.2	372	7	US-11-054-515-948	Sequence 948, App
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377	88	4.2	377	7	US-11-054-515-1240	Sequence 1240, App
378	88	4.2	378	1	PCT-US04-23166A-709	Sequence 709, App
379	88	4.2	379	6	US-10-450-763-53444	Sequence 53444, A
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383	87.5	4.2	383	7	US-11-033-545-505	Sequence 505, App
384	87.5	4.2	384	7	US-11-054-515-2112	Sequence 2112, App
385	87.5	4.2	385	7	US-11-054-515-2054	Sequence 2054, App
386	87.5	4.2	386	7	US-11-054-515-1985	Sequence 1985, App
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391	87.5	4.2	720	6	US-10-450-763-60358	Sequence 60358, A
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393	87.5	4.2	1907	6	US-10-712-892A-34	Sequence 34, Appl
394	87	4.1	244	7	US-11-054-515-1845	Sequence 1845, Ap
395	87	4.1	247	7	US-11-054-515-1328	Sequence 1328, Ap
396	87	4.1	248	1	PCT-US04-38197-275	Sequence 275, App
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398	87	4.1	249	7	US-11-054-515-472	Sequence 472, App
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404	87	4.1	548	7	US-11-028-058-11	Sequence 11, Appl
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417	86.5	4.1	251	7	US-11-054-515-1011	Sequence 1011, Ap
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419	86.5	4.1	251	7	US-11-054-515-1072	Sequence 1072, Ap
420	86.5	4.1	251	7	US-11-054-515-1076	Sequence 1076, Ap
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422	86.5	4.1	251	7	US-11-054-515-1086	Sequence 1086, Ap
423	86.5	4.1	251	7	US-11-054-515-1143	Sequence 1143, Ap
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426	86.5	4.1	251	7	US-11-054-515-1396	Sequence 1396, Ap
427	86.5	4.1	251	7	US-11-054-515-1769	Sequence 1769, Ap
428	86.5	4.1	253	7	US-11-054-515-1829	Sequence 1829, Ap
429	86.5	4.1	256	7	US-11-054-515-1855	Sequence 1855, Ap
430	86.5	4.1	258	7	US-11-054-515-1255	Sequence 1255, Ap
431	86.5	4.1	568	8	US-60-643-717-3396	Sequence 3396, Ap
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435	86	4.1	243	7	US-11-054-515-1863	Sequence 1863, Ap
436	86	4.1	247	6	US-10-450-763-49654	Sequence 49654, A
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443	86	4.1	253	7	US-11-054-515-1227	Sequence 1227, Ap
444	86	4.1	255	1	PCT-US04-38197-278	Sequence 278, App
445	86	4.1	262	1	PCT-US04-38197-280	Sequence 280, App
446	86	4.1	590	7	US-11-058-709-12	Sequence 12, Appl
447	86	4.1	656	7	US-11-030-653-38	Sequence 38, Appl
448	86	4.1	713	7	US-11-030-653-26	Sequence 26, Appl
449	86	4.1	1336	6	US-10-712-892A-33	Sequence 33, Appl
450	85.5	4.1	170	6	US-10-450-763-51714	Sequence 51714, A
451	85.5	4.1	237	7	US-11-054-515-2006	Sequence 2006, Ap
452	85.5	4.1	237	7	US-11-054-515-2036	Sequence 2036, Ap
453	85.5	4.1	243	7	US-11-054-515-2056	Sequence 2056, Ap
454	85.5	4.1	248	7	US-11-054-515-1890	Sequence 1890, Ap
455	85.5	4.1	250	7	US-11-054-515-1723	Sequence 1723, Ap
456	85.5	4.1	251	7	US-11-054-515-875	Sequence 875, App
457	85.5	4.1	251	7	US-11-054-515-879	Sequence 879, App
458	85.5	4.1	251	7	US-11-054-515-886	Sequence 886, App
459	85.5	4.1	251	7	US-11-054-515-975	Sequence 975, App
460	85.5	4.1	251	7	US-11-054-515-978	Sequence 978, App
461	85.5	4.1	251	7	US-11-054-515-1055	Sequence 1055, Ap
462	85.5	4.1	251	7	US-11-054-515-1057	Sequence 1057, Ap
463	85.5	4.1	251	7	US-11-054-515-1059	Sequence 1059, Ap
464	85.5	4.1	251	7	US-11-054-515-1064	Sequence 1064, Ap
465	85.5	4.1	251	7	US-11-054-515-1078	Sequence 1078, Ap
466	85.5	4.1	251	7	US-11-054-515-1079	Sequence 1079, Ap
467	85.5	4.1	251	7	US-11-054-515-1085	Sequence 1085, Ap
468	85.5	4.1	251	7	US-11-054-515-1176	Sequence 1176, Ap
469	85.5	4.1	251	7	US-11-054-515-1187	Sequence 1187, Ap
470	85.5	4.1	251	7	US-11-054-515-1338	Sequence 1338, Ap
471	85.5	4.1	251	7	US-11-054-515-1345	Sequence 1345, Ap
472	85.5	4.1	251	7	US-11-054-515-1408	Sequence 1408, Ap
473	85.5	4.1	251	7	US-11-054-515-1437	Sequence 1437, Ap
474	85.5	4.1	251	7	US-11-054-515-1478	Sequence 1478, Ap
475	85.5	4.1	251	7	US-11-054-515-1587	Sequence 1587, Ap
476	85.5	4.1	251	7	US-11-054-515-1749	Sequence 1749, Ap
477	85.5	4.1	251	7	US-11-054-515-1752	Sequence 1752, Ap
478	85.5	4.1	251	7	US-11-054-515-1758	Sequence 1758, Ap
479	85.5	4.1	251	7	US-11-054-515-1763	Sequence 1763, Ap
480	85.5	4.1	251	7	US-11-054-515-1768	Sequence 1768, Ap
481	85.5	4.1	251	7	US-11-054-515-1775	Sequence 1775, Ap
482	85.5	4.1	251	7	US-11-054-515-1792	Sequence 1792, Ap
483	85.5	4.1	251	7	US-11-054-515-1798	Sequence 1798, Ap
484	85.5	4.1	251	7	US-11-054-515-1803	Sequence 1803, Ap
485	85.5	4.1	251	7	US-11-054-515-1810	Sequence 1810, Ap
486	85.5	4.1	251	7	US-11-054-515-1822	Sequence 1822, Ap
487	85.5	4.1	251	7	US-11-054-515-1825	Sequence 1825, Ap
488	85.5	4.1	251	7	US-11-054-515-1827	Sequence 1827, Ap
489	85.5	4.1	252	7	US-11-054-515-1475	Sequence 1475, Ap
490	85.5	4.1	252	7	US-11-054-515-1500	Sequence 1500, Ap
491	85.5	4.1	254	7	US-11-054-515-1893	Sequence 1893, Ap
492	85.5	4.1	257	7	US-11-054-515-1283	Sequence 1283, Ap
493	85.5	4.1	343	1	PCT-US03-2596-2	Sequence 2, Appli
494	85.5	4.1	479	6	US-10-450-763-51419	Sequence 51419, A
495	85.5	4.1	1375	6	US-10-450-763-32231	Sequence 32231, A
496	85.5	4.1	1495	6	US-10-450-763-34736	Sequence 34736, A
497	85	4.1	234	8	US-60-651-509-269	Sequence 269, App
498	85	4.1	240	7	US-11-054-515-2113	Sequence 2113, Ap
499	85	4.1	247	7	US-11-054-515-1492	Sequence 1492, Ap
500	85	4.1	247	7	US-11-054-515-1711	Sequence 1711, Ap
501	85	4.1	249	7	US-11-054-515-499	Sequence 499, App
502	85	4.1	249	7	US-11-054-515-737	Sequence 737, App
503	85	4.1	249	7	US-11-054-515-1299	Sequence 1299, Ap
504	85	4.1	252	7	US-11-054-515-1787	Sequence 1787, Ap
505	85	4.1	258	1	PCT-US04-38197-155	Sequence 155, App
506	85	4.1	258	7	US-11-054-515-1265	Sequence 1265, Ap
507	85	4.1	295	7	US-11-040-706-5	Sequence 5, Appli
508	85	4.1	479	6	US-10-450-763-48879	Sequence 48879, A
509	85	4.1	479	6	US-10-489-448-2817	Sequence 2817, Ap
510	85	4.1	512	7	US-11-032-232-8	Sequence 8, Appli
511	85	4.1	532	8	US-60-651-509-417	Sequence 417, App
512	85	4.1	570	8	US-60-651-509-415	Sequence 415, App
513	85	4.1	583	8	US-60-651-509-416	Sequence 416, App
514	85	4.1	651	6	US-10-450-763-43249	Sequence 43249, A
515	85	4.1	2409	6	US-10-852-335A-184	Sequence 184, App
516	84.5	4.0	238	7	US-11-054-515-1931	Sequence 1931, Ap
517	84.5	4.0	242	7	US-11-054-515-2106	Sequence 2106, Ap
518	84.5	4.0	244	7	US-11-054-515-1582	Sequence 1582, Ap
519	84.5	4.0	245	7	US-11-054-515-1550	Sequence 1550, Ap
520	84.5	4.0	248	7	US-11-054-515-970	Sequence 970, App
521	84.5	4.0	250	7	US-11-054-515-1722	Sequence 1722, Ap
522	84.5	4.0	251	7	US-11-054-515-1132	Sequence 1132, Ap
523	84.5	4.0	251	7	US-11-054-515-1542	Sequence 1542, Ap
524	84.5	4.0	251	7	US-11-054-515-1706	Sequence 1706, Ap
525	84.5	4.0	251	7	US-11-054-515-1747	Sequence 1747, Ap
526	84.5	4.0	251	7	US-11-054-515-1795	Sequence 1795, Ap
527	84.5	4.0	251	7	US-11-054-515-1824	Sequence 1824, Ap
528	84.5	4.0	251	7	US-11-054-515-1833	Sequence 1833, Ap
529	84.5	4.0	259	1	PCT-US04-38197-161	Sequence 161, App
530	84.5	4.0	262	1	PCT-US04-38197-162	Sequence 162, App
531	84.5	4.0	266	1	PCT-US04-38197-163	Sequence 163, App
532	84.5	4.0	423	6	US/10/013	Sequence 8, Appli
533	84.5	4.0	504	6	US-10-450-763-48871	Sequence 48871, A
534	84.5	4.0	543	6	US-10-495-664-3	Sequence 3, Appli
535	84.5	4.0	568	8	US-60-643-717-7278	Sequence 7278, Ap
536	84.5	4.0	568	8	US-60-643-717-17558	Sequence 17558, A

537	84.5	4.0	794	6	US-10-499-353A-545	Sequence 545, App
538	84.5	4.0	1142	6	US-10-287-436A-564	Sequence 564, App
539	84	4.0	148	6	US-10-450-763-43242	Sequence 43242, A
540	84	4.0	163	6	US-10-450-763-53696	Sequence 53696, A
541	84	4.0	240	7	US-11-054-515-2041	Sequence 2041, Ap
542	84	4.0	240	7	US-11-054-515-2105	Sequence 2105, Ap
543	84	4.0	241	7	US-11-054-515-1932	Sequence 1932, Ap
544	84	4.0	247	7	US-11-054-515-1099	Sequence 1099, Ap
545	84	4.0	247	7	US-11-054-515-1527	Sequence 1527, Ap
546	84	4.0	249	7	US-11-054-515-436	Sequence 436, App
547	84	4.0	249	7	US-11-054-515-495	Sequence 495, App
548	84	4.0	250	7	US-11-054-515-1367	Sequence 1367, Ap
549	84	4.0	251	7	US-11-054-515-1832	Sequence 1832, Ap
550	84	4.0	264	1	PCT-US04-38197-31	Sequence 31, Appl
551	84	4.0	718	1	PCT-US05-02350-534	Sequence 534, App
552	84	4.0	718	7	US-11-043-770-534	Sequence 534, App
553	84	4.0	733	1	PCT-US05-02350-533	Sequence 533, App
554	84	4.0	733	7	US-11-043-770-533	Sequence 533, Appl
555	84	4.0	1130	8	US-60-643-717-2342	Sequence 2342, Ap
556	83.5	4.0	242	7	US-11-054-515-2021	Sequence 2021, Ap
557	83.5	4.0	244	7	US-11-054-515-2058	Sequence 2058, Ap
558	83.5	4.0	245	7	US-11-054-515-1826	Sequence 1826, Ap
559	83.5	4.0	246	7	US-11-054-515-1630	Sequence 1630, Ap
560	83.5	4.0	246	7	US-11-054-515-1996	Sequence 1996, Ap
561	83.5	4.0	249	7	US-11-054-515-1817	Sequence 1817, Ap
562	83.5	4.0	249	7	US-11-054-515-2065	Sequence 2065, Ap
563	83.5	4.0	250	7	US-11-054-515-1228	Sequence 1228, Ap
564	83.5	4.0	251	7	US-11-054-515-943	Sequence 943, App
565	83.5	4.0	251	7	US-11-054-515-1051	Sequence 1051, Ap
566	83.5	4.0	251	7	US-11-054-515-1068	Sequence 1068, Ap
567	83.5	4.0	251	7	US-11-054-515-1106	Sequence 1106, Ap
568	83.5	4.0	251	7	US-11-054-515-1292	Sequence 1292, Ap
569	83.5	4.0	251	7	US-10-499-352A-480	Sequence 480, Appl
570	83.5	4.0	253	7	US-11-054-515-1556	Sequence 1556, Ap
571	83.5	4.0	253	7	US-11-054-515-1509	Sequence 1509, Ap
572	83.5	4.0	288	7	US-11-054-515-2101	Sequence 2101, Ap
573	83.5	4.0	432	1	PCT-US04-15399A-16	Sequence 16, Appl1
574	83.5	4.0	673	7	US-11-043-591-94	Sequence 94, Appl
575	83.5	4.0	726	6	US-10-499-352A-480	Sequence 480, App
576	83.5	4.0	737	6	US-10-499-352A-476	Sequence 476, App
577	83.5	4.0	911	1	PCT-US04-42360-2545	Sequence 2545, Ap
578	83.5	4.0	3011	1	PCT-US04-09510-1710	Sequence 1710, Ap
579	83	4.0	236	6	US-10-450-763-49657	Sequence 49657, A
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581	83	4.0	248	7	US-11-054-515-913	Sequence 913, App
582	83	4.0	248	7	US-11-054-515-921	Sequence 921, App
583	83	4.0	249	7	US-11-054-515-376	Sequence 376, App
584	83	4.0	249	7	US-11-054-515-496	Sequence 496, App
585	83	4.0	249	7	US-11-054-515-586	Sequence 586, App
586	83	4.0	249	7	US-11-054-515-665	Sequence 665, App
587	83	4.0	249	7	US-11-054-515-732	Sequence 732, App
588	83	4.0	249	7	US-11-054-515-788	Sequence 788, App
589	83	4.0	251	7	US-11-043-591-108	Sequence 108, App
590	83	4.0	251	7	US-11-054-515-1140	Sequence 1140, Ap
591	83	4.0	251	7	US-11-054-515-1149	Sequence 1149, Ap
592	83	4.0	251	7	US-11-054-515-1784	Sequence 1784, Ap
593	83	4.0	252	7	US-11-043-591-104	Sequence 104, App
594	83	4.0	252	7	US-11-054-515-1541	Sequence 1541, Ap
595	83	4.0	256	7	US-11-054-515-2119	Sequence 2119, Ap
596	83	4.0	260	7	US-11-043-591-106	Sequence 106, App
597	83	4.0	348	6	US-10-450-763-40182	Sequence 40182, A
598	83	4.0	392	6	US-10-450-763-48881	Sequence 48881, A
599	83	4.0	420	7	US-11-021-825-121	Sequence 121, App
600	83	4.0	445	7	US-11-027-399-4414	Sequence 4414, Ap
601	83	4.0	445	7	US-11-027-843-4414	Sequence 4414, Ap
602	83	4.0	445	7	US-11-027-878-4414	Sequence 4414, Ap
603	83	4.0	445	7	US-11-028-169-4414	Sequence 4414, Ap
604	83	4.0	445	7	US-11-028-204-4414	Sequence 4414, Ap
605	83	4.0	445	7	US-11-027-877-4414	Sequence 4414, Ap
606	83	4.0	445	7	US-11-027-879-4414	Sequence 4414, Ap
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608	83	4.0	445	7	US-11-027-802-4414	Sequence 4414, Ap
609	83	4.0	445	7	US-11-027-890-4414	Sequence 4414, Ap
610	83	4.0	445	7	US-11-027-892-4414	Sequence 4414, Ap
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612	83	4.0	445	7	US-11-028-197-4414	Sequence 4414, Ap
613	83	4.0	445	7	US-11-028-844-4414	Sequence 4414, Ap
614	83	4.0	445	7	US-11-028-050-4414	Sequence 4414, Ap
615	83	4.0	445	7	US-11-028-457-4414	Sequence 4414, Ap
616	83	4.0	445	7	US-11-027-891-4414	Sequence 4414, Ap
617	83	4.0	445	7	US-11-028-291-4414	Sequence 4414, Ap
618	83	4.0	445	7	US-11-028-458-4414	Sequence 4414, Ap
619	83	4.0	498	7	US-11-050-926-328	Sequence 328, App
620	83	4.0	569	6	US-10-450-763-58212	Sequence 58212, A
621	83	4.0	889	6	US-10-450-763-54238	Sequence 54238, A
622	83	4.0	1131	6	US-10-450-763-48943	Sequence 48943, A
623	82.5	3.9	131	6	US-10-494-333-84	Sequence 84, Appl
624	82.5	3.9	203	1	PCT-US04-43468-10	Sequence 10, Appl
625	82.5	3.9	237	7	US-11-054-515-2111	Sequence 2111, Ap
626	82.5	3.9	237	7	US-11-054-515-2118	Sequence 2118, Ap
627	82.5	3.9	242	7	US-11-054-515-2084	Sequence 2084, Ap
628	82.5	3.9	247	7	US-11-054-515-1703	Sequence 1703, Ap
629	82.5	3.9	249	7	US-11-054-515-1202	Sequence 1202, Ap
630	82.5	3.9	251	7	US-11-054-515-1473	Sequence 1473, Ap
631	82.5	3.9	251	7	US-11-054-515-1783	Sequence 1783, Ap
632	82.5	3.9	251	7	US-11-054-515-1793	Sequence 1793, Ap
633	82.5	3.9	251	7	US-11-054-515-1840	Sequence 1840, Ap
634	82.5	3.9	254	7	US-11-054-515-1865	Sequence 1865, Ap
635	82.5	3.9	263	1	PCT-US04-38197-152	Sequence 152, App
636	82.5	3.9	363	6	US-10-450-763-51772	Sequence 51772, A
637	82.5	3.9	466	6	US-10-184-644-316	Sequence 316, App
638	82.5	3.9	466	7	US-11-025-607-267	Sequence 267, App
639	82.5	3.9	466	7	US-11-048-692-37	Sequence 37, Appl
640	82.5	3.9	491	6	US-10-450-763-56424	Sequence 56424, A
641	82.5	3.9	551	7	US-11-041-419-33	Sequence 33, Appl
642	82.5	3.9	1000	1	PCT-US05-04041-374	Sequence 374, App
643	82.5	3.9	1003	1	PCT-US05-04041-378	Sequence 378, App
644	82.5	3.9	1193	8	US-60-643-717-14095	Sequence 14095, A
645	82	3.9	216	7	US-11-021-951-159	Sequence 159, App
646	82	3.9	238	7	US-11-054-515-1907	Sequence 1907, Ap
647	82	3.9	240	7	US-11-054-515-2030	Sequence 2030, Ap
648	82	3.9	240	7	US-11-054-515-2044	Sequence 2044, Ap
649	82	3.9	241	7	US-11-054-515-2008	Sequence 2008, Ap
650	82	3.9	241	7	US-11-054-515-2031	Sequence 2031, Ap
651	82	3.9	243	7	US-11-054-515-1940	Sequence 1940, Ap
652	82	3.9	244	7	US-11-054-515-1372	Sequence 1372, Ap
653	82	3.9	245	7	US-11-054-515-1615	Sequence 1615, Ap
654	82	3.9	248	6	US-10-450-763-56711	Sequence 56711, A
655	82	3.9	248	7	US-11-054-515-1982	Sequence 1982, Ap
656	82	3.9	249	7	US-11-054-515-357	Sequence 357, App
657	82	3.9	249	7	US-11-054-515-362	Sequence 362, App
658	82	3.9	249	7	US-11-054-515-393	Sequence 393, App
659	82	3.9	249	7	US-11-054-515-506	Sequence 506, App
660	82	3.9	249	7	US-11-054-515-560	Sequence 560, App
661	82	3.9	249	7	US-11-054-515-604	Sequence 604, App
662	82	3.9	249	7	US-11-054-515-642	Sequence 642, App
663	82	3.9	249	7	US-11-054-515-659	Sequence 659, App
664	82	3.9	249	7	US-11-054-515-745	Sequence 745, App
665	82	3.9	249	7	US-11-054-515-775	Sequence 775, App
666	82	3.9	249	7	US-11-054-515-783	Sequence 783, App
667	82	3.9	249	7	US-11-054-515-787	Sequence 787, App
668	82	3.9	249	7	US-11-054-515-1570	Sequence 1570, Ap
669	82	3.9	249	7	US-11-054-515-1725	Sequence 1725, Ap
670	82	3.9	249	7	US-11-054-515-2033	Sequence 2033, Ap
671	82	3.9	250	8	US-60-643-717-7334	Sequence 7334, Ap
672	82	3.9	252	7	US-11-054-515-897	Sequence 897, App
673	82	3.9	252	7	US-11-054-515-1016	Sequence 1016, Ap
674	82	3.9	252	7	US-11-054-515-1575	Sequence 1575, Ap
675	82	3.9	252	7	US-11-054-515-1695	Sequence 1695, Ap
676	82	3.9	252	7	US-11-054-515-1874	Sequence 1874, Ap
677	82	3.9	253	7	US-11-054-515-1199	Sequence 1199, Ap
678	82	3.9	253	7	US-11-054-515-1858	Sequence 1858, Ap
679	82	3.9	253	7	US-11-054-515-1987	Sequence 1987, Ap
680	82	3.9	258	1	PCT-US04-38197-151	Sequence 151, App
681	82	3.9	259	7	US-11-054-515-1262	Sequence 1262, App
682	82	3.9	620	7	US-11-048-692-11	Sequence 11, Appl

683	82	3.9	661	7	US-11-043-591-186	Sequence 186, App
684	82	3.9	709	6	US-10-450-763-51173	Sequence 51173, A
685	82	3.9	762	7	US-11-035-599-28	Sequence 28, Appl
686	82	3.9	1121	8	US-60-643-717-11126	Sequence 11126, A
687	82	3.9	1231	6	US-10-450-763-48035	Sequence 48035, A
688	82	3.9	1231	6	US-10-450-763-54756	Sequence 54756, A
689	82	3.9	1663	6	US-10-450-763-41525	Sequence 41525, A
690	81.5	3.9	237	7	US-11-054-515-2104	Sequence 2104, Ap
691	81.5	3.9	241	7	US-11-054-515-1303	Sequence 1303, Ap
692	81.5	3.9	248	7	US-11-054-515-1662	Sequence 1662, Ap
693	81.5	3.9	249	7	US-11-054-515-1009	Sequence 1009, Ap
694	81.5	3.9	250	7	US-11-054-515-1203	Sequence 1203, Ap
695	81.5	3.9	250	7	US-11-054-515-1563	Sequence 1563, Ap
696	81.5	3.9	250	7	US-11-054-515-1564	Sequence 1564, Ap
697	81.5	3.9	733	7	US-11-031-175-13857	Sequence 13857, A
698	81.5	3.9	995	6	US-10-450-763-52543	Sequence 52543, A
699	81	3.9	240	7	US-11-054-515-2016	Sequence 2016, Ap
700	81	3.9	240	7	US-11-054-515-2048	Sequence 2048, Ap
701	81	3.9	243	7	US-11-054-515-2014	Sequence 2014, Ap
702	81	3.9	243	7	US-11-054-515-2057	Sequence 2057, Ap
703	81	3.9	247	7	US-11-054-515-878	Sequence 878, App
704	81	3.9	247	7	US-11-054-515-1090	Sequence 1090, Ap
705	81	3.9	247	7	US-11-054-515-1269	Sequence 1269, Ap
706	81	3.9	249	7	US-11-054-515-349	Sequence 349, App
707	81	3.9	249	7	US-11-054-515-373	Sequence 373, App
708	81	3.9	249	7	US-11-054-515-434	Sequence 434, App
709	81	3.9	249	7	US-11-054-515-609	Sequence 609, App
710	81	3.9	249	7	US-11-054-515-670	Sequence 670, App
711	81	3.9	249	7	US-11-054-515-712	Sequence 712, App
712	81	3.9	249	7	US-11-054-515-739	Sequence 739, App
713	81	3.9	249	7	US-11-054-515-754	Sequence 754, App
714	81	3.9	249	7	US-11-054-515-764	Sequence 764, App
715	81	3.9	249	7	US-11-054-515-777	Sequence 777, App
716	81	3.9	249	7	US-11-054-515-780	Sequence 780, App
717	81	3.9	249	7	US-11-054-515-790	Sequence 790, App
718	81	3.9	249	7	US-11-054-515-822	Sequence 822, App
719	81	3.9	250	6	US-10-521-109-6	Sequence 6, Appli
720	81	3.9	251	7	US-11-054-515-1395	Sequence 1395, Ap
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722	81	3.9	252	7	US-11-054-515-1135	Sequence 1135, Ap
723	81	3.9	252	7	US-11-054-515-1163	Sequence 1163, Ap
724	81	3.9	252	7	US-11-054-515-1236	Sequence 1236, Ap
725	81	3.9	253	7	US-11-054-515-1499	Sequence 1499, Ap
726	81	3.9	253	7	US-11-054-515-1848	Sequence 1848, Ap
727	81	3.9	253	7	US-11-054-515-1951	Sequence 1951, Ap
728	81	3.9	258	7	US-11-054-515-1266	Sequence 1266, Ap
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733	81	3.9	3419	1	PCT-US04-42360-180	Sequence 180, App
734	80.5	3.8	218	5	US-09-791-153E-50	Sequence 50, Appl
735	80.5	3.8	238	6	US-10-496-861-7	Sequence 7, Appli
736	80.5	3.8	239	7	US-11-054-515-2035	Sequence 2035, Ap
737	80.5	3.8	241	7	US-11-054-515-1911	Sequence 1911, Ap
738	80.5	3.8	242	7	US-11-054-515-1844	Sequence 1844, Ap
739	80.5	3.8	246	7	US-11-054-515-1655	Sequence 1655, Ap
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741	80.5	3.8	248	7	US-11-054-515-1403	Sequence 1403, Ap
742	80.5	3.8	248	7	US-11-054-515-1665	Sequence 1665, Ap
743	80.5	3.8	250	7	US-11-054-515-1017	Sequence 1017, Ap
744	80.5	3.8	250	7	US-11-054-515-1647	Sequence 1647, Ap
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746	80.5	3.8	251	7	US-11-054-515-1020	Sequence 1020, Ap
747	80.5	3.8	251	7	US-11-054-515-1077	Sequence 1077, Ap
748	80.5	3.8	251	7	US-11-054-515-1343	Sequence 1343, Ap
749	80.5	3.8	254	7	US-11-054-515-1846	Sequence 1846, Ap
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756	80.5	3.8	570	8	US-60-643-717-19044	Sequence 19044, A
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758	80.5	3.8	759	6	US-10-450-763-52306	Sequence 52306, A
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764	80	3.8	242	7	US-11-054-515-1438	Sequence 1438, Ap
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766	80	3.8	244	7	US-11-054-515-2069	Sequence 2069, Ap
767	80	3.8	246	7	US-11-054-515-1286	Sequence 1286, Ap
768	80	3.8	247	7	US-11-054-515-720	Sequence 720, App
769	80	3.8	247	7	US-11-054-515-1384	Sequence 1384, Ap
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771	80	3.8	248	7	US-11-054-515-1323	Sequence 1323, Ap
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773	80	3.8	248	7	US-11-054-515-1456	Sequence 1456, Ap
774	80	3.8	249	7	US-11-054-515-381	Sequence 381, App
775	80	3.8	249	7	US-11-054-515-386	Sequence 386, App
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778	80	3.8	249	7	US-11-054-515-418	Sequence 418, App
779	80	3.8	249	7	US-11-054-515-431	Sequence 431, App
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786	80	3.8	249	7	US-11-054-515-577	Sequence 566, App
787	80	3.8	249	7	US-11-054-515-566	Sequence 577, App
788	80	3.8	249	7	US-11-054-515-653	Sequence 653, App
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790	80	3.8	249	7	US-11-054-515-735	Sequence 735, App
791	80	3.8	249	7	US-11-054-515-746	Sequence 746, App
792	80	3.8	249	7	US-11-054-515-793	Sequence 793, App
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794	80	3.8	249	7	US-11-054-515-807	Sequence 807, App
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797	80	3.8	251	7	US-11-054-515-1048	Sequence 1048, Ap
798	80	3.8	252	7	US-11-054-515-1490	Sequence 1490, Ap
799	80	3.8	253	7	US-11-054-515-1259	Sequence 1259, Ap
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803	80	3.8	394	6	US-10-450-763-51564	Sequence 51564, A
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834	79.5	3.8	1663	PCT-US04-42360-424	Sequence 424, App
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839	79	3.8	242	US-11-054-515-2046	Sequence 2046, Ap
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844	79	3.8	249	US-11-054-515-351	Sequence 351, App
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847	79	3.8	249	US-11-054-515-476	Sequence 476, App
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853	79	3.8	249	US-11-054-515-589	Sequence 589, App
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869	79	3.8	251	US-11-054-515-998	Sequence 998, App
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871	79	3.8	252	US-11-043-591-113	Sequence 113, App
872	79	3.8	252	US-11-054-515-1658	Sequence 1658, Ap
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877	79	3.8	378	US-60-643-717-15158	Sequence 15158, A
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897	78.5	3.7	256	US-11-054-515-1604	Sequence 1604, Ap
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909	78.5	3.7	702	US-11-035-599-53	Sequence 53, Appl
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955	78	3.7	249	US-11-054-515-606	Sequence 606, App
956	78	3.7	249	US-11-054-515-610	Sequence 610, App
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962	78	3.7	249	US-11-054-515-697	Sequence 697, App
963	78	3.7	249	US-11-054-515-765	Sequence 765, App
964	78	3.7	249	US-11-054-515-766	Sequence 766, App
965	78	3.7	249	US-11-054-515-769	Sequence 769, App
966	78	3.7	249	US-11-054-515-809	Sequence 809, App
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973	78	3.7	253	US-11-054-515-1167	Sequence 1167, Ap
974	78	3.7	253	US-11-054-515-1375	Sequence 1375, Ap

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976	78	3.7	253	7	US-11-054-515-1859	Sequence 1859, Ap
977	78	3.7	253	7	US-11-054-515-1895	Sequence 1895, Ap
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982	78	3.7	335	6	US-10-842-011A-2	Sequence 2, Appli
983	78	3.7	335	6	US-10-184-644-192	Sequence 192, App
984	78	3.7	404	6	US-10-450-763-39978	Sequence 39978, A
985	78	3.7	620	6	US-10-450-763-35429	Sequence 35429, A
986	78	3.7	1183	6	US-10-937-758A-45	Sequence 45, Appl
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992	77.5	3.7	247	7	US-11-054-515-1018	Sequence 1018, Ap
993	77.5	3.7	248	7	US-11-054-515-967	Sequence 967, App
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1003	77.5	3.7	253	7	US-11-054-515-1835	Sequence 1835, Ap
1004	77.5	3.7	254	7	US-11-054-515-1350	Sequence 1350, Ap
1005	77.5	3.7	254	7	US-11-054-515-1866	Sequence 1866, Ap
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1186	76	3.6	123	6	US-10-523-444-4	Sequence 4, Appl1	1259	75	3.6	249	7	US-11-054-515-448	Sequence 448, App
1187	75.5	3.6	237	7	US-11-054-515-2019	Sequence 2019, Ap	1260	75	3.6	249	7	US-11-054-515-465	Sequence 465, App
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1269	75	3.6	249	7	US-11-054-515-549	Sequence 549, App	1342	75	3.6	396	7	US-11-027-891-2778	Sequence 2778, Ap
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ALIGNMENTS

RESULT 1
US-09-978-191C-52
Sequence 52, Application US/09978191C
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 623
; SEQ ID NO 52
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-191C-52
```

Query Match 80.5%; Score 1688; DB 5; length 321;
Best Local Similarity 100.0%; Pred. No. 8.8e-136;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLOLSTLEMDDRSHTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLOLSTLEMDDRSHTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFIVPQGMRLISLQCCQARGSPPISTIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFIVPQGMRLISLQCCQARGSPPISTIWKQ 180
QY 181 QTNNOEPKIVATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSDIVKFVVKDSSKLKTK 240
Db 181 QTNNOEPKIVATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSDIVKFVVKDSSKLKTK 240
QY 241 TEAPTMITYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPFVAIILISLCMVVET 300
Db 241 TEAPTMITYPLKATSTVKQSWDWTMDGYLGETSAGPKSLPFVAIILISLCMVVET 300
QY 301 MAYIMLCRKTSQOEHVYEAAR 321
Db 301 MAYIMLCRKTSQOEHVYEAAR 321
```

```
RESULT 2
US-10-986-822-6
; Sequence 6, Application US/10986822
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: YUE, Henry
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: GORGONE, Gina A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: PROTEIN TRANSPORT-ASSOCIATED MOLECULES
; FILE REFERENCE: PF-0577 PCT
; CURRENT APPLICATION NUMBER: US/10/986,822
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/763,902
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/098,206
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No:1871275CD1
US-10-986-822-6
```

Query Match 41.5%; Score 870; DB 6; length 175;
Best Local Similarity 64.7%; Pred. No. 1.2e-66;
Matches 174; Conservative 0; Mismatches 1; Indels 94; Gaps 1;

```
QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLOLSTLEMDDRSHTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLOLSTLEMDDRSHTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTGSGYGFIVPQGMRLISLQCCQARGSPPISTIWKQ 180
Db 121 DGNQVVRDKITELRVQ-----136
QY 181 QTNNOEPKIVATLSTLLFKPAVIADSGSYFCTAKQGVSEQHSDIVKFVVKDSSKLKTK 240
Db 137 -----KHSSKLKTK 146
QY 241 TEAPTMITYPLKATSTVKQSWDWTMDG 269
Db 147 TEAPTMITYPLKATSTVKQSWDWTMDG 175
```

```
RESULT 3
US-10-523-834-330
; Sequence 330, Application US/10523834
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Sun, Yongming
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P
; FILE REFERENCE: DEX-0443
; CURRENT APPLICATION NUMBER: US/10/523,834
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/401,469
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 396
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 330
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-523-834-330
```

Query Match 8.5%; Score 178.5; DB 6; length 335;
Best Local Similarity 26.5%; Pred. No. 1.5e-07;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

```
QY 1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 17 LAILLCSIALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW---- 62
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHK-----VPGDVSLOLSTLEMDDRSHTCEV 115
Db 63 -----KFDQGDITRLVLCYNNKITASIEDRVTFPLPTGITFKSVTRE--DTGYTCMV 111
QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTGSGYGFIVPQGMRLISLQCCQAR-GSPPI 174
Db 112 SEEGNSYGEVVKVLIVL---VPPSKPTVINIPS---SATIGNRAVLTCSEQDGSPPSE 163
QY 175 YIWK---QQTN-----NOEPKIVATLSTLLFKPAVIADSGSYFCTAKQGVSEQH 222
Db 164 YTFPKDGIWMPITNPKSTRAFSNSSYVLNPTTGLVFDPLSASDTEYSCEARNGYGTGMT 223
QY 223 SDIVK 227
Db 224 SNAVR 228
```

```
RESULT 4
US-10-155-282B-11
; Sequence 11, Application US/10155282B
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; APPLICANT: Freimuth, Paul I
; TITLE OF INVENTION: Recombinant Soluble Adenovirus Receptor
; FILE REFERENCE: BSA 02-14
; CURRENT APPLICATION NUMBER: US/10/155,282B
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/236,423
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-155-282B-11
```

```
Query Match          7.6%; Score 159; DB 6; Length 365;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches 81; Conservative 49; Mismatches 119; Indels 100; Gaps 20;
```

```
QY      1 MGIILGILLGLHGLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQ 51
      1 MALLLCFVLL--CGVVDFAARSLITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLD---- 54
DB
QY      52 VLVKWLNVQRGS----DPVTIFLRDSSGDHIQAKY---QGRLVHSHK--VPGDVSLOLST 102
      55 --IEWLISPADNQKVDQVILLY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
DB
QY      103 LEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPT---VTTGSGYGFVTPQG 158
      110 LQLSDIGTYQCKVK-KAPG-----VANKKIHLVVLVKGSGARCYVDG-----EEIG 155
DB
QY      159 MRISLQCCQAR-GSPPISYIWKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAK 214
      156 SDFKICEPKESGLPQYEWQKLSDSQKMPSTWLAEMTSSVISKNASSEYSGTYSCTVR 215
DB
QY      215 GOVGEQHSIDIVKFFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTMDGYLGCT 274
      216 NRVGSDQ-----CLRLNVPPSN-----KA-----GLIAGA 242
DB
QY      275 SAGPGKSLPVFAIILISLCMVFTMAYIMLCRKTSQOEHVYEABARAH 323
      243 IIG---TLALALIGLIIFCC-----RKKRREKEKEKEVHN 275
DB
```

```
RESULT 5
US-60-651-509-101
; Sequence 101, Application US/60651509
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CLO01578
; CURRENT APPLICATION NUMBER: US/60/651,509
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 1940
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 101
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-509-101
```

```
Query Match          7.6%; Score 159; DB 8; Length 365;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches 81; Conservative 49; Mismatches 119; Indels 100; Gaps 20;
```

```
QY      1 MGIILGILLGLHGLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQ 51
      1 MALLLCFVLL--CGVVDFAARSLITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLD---- 54
DB
```

```
DB      1 MALLLCFVLL--CGVVDFAARSLITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLD---- 54
QY      52 VLVKWLNVQRGS----DPVTIFLRDSSGDHIQAKY---QGRLVHSHK--VPGDVSLOLST 102
      55 --IEWLISPADNQKVDQVILLY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
DB
QY      103 LEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPT---VTTGSGYGFVTPQG 158
      110 LQLSDIGTYQCKVK-KAPG-----VANKKIHLVVLVKGSGARCYVDG-----EEIG 155
DB
QY      159 MRISLQCCQAR-GSPPISYIWKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAK 214
      156 SDFKICEPKESGLPQYEWQKLSDSQKMPSTWLAEMTSSVISKNASSEYSGTYSCTVR 215
DB
QY      215 GOVGEQHSIDIVKFFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTMDGYLGCT 274
      216 NRVGSDQ-----CLRLNVPPSN-----KA-----GLIAGA 242
DB
QY      275 SAGPGKSLPVFAIILISLCMVFTMAYIMLCRKTSQOEHVYEABARAH 323
      243 IIG---TLALALIGLIIFCC-----RKKRREKEKEKEVHN 275
DB
```

```
RESULT 6
US-60-651-509-103
; Sequence 103, Application US/60651509
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CLO01578
; CURRENT APPLICATION NUMBER: US/60/651,509
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 1940
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 103
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-509-103
```

```
Query Match          7.6%; Score 159; DB 8; Length 365;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches 81; Conservative 49; Mismatches 119; Indels 100; Gaps 20;
```

```
QY      1 MGIILGILLGLHGLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY-----DPLQGYTQ 51
      1 MALLLCFVLL--CGVVDFAARSLITTPPEEMIEKAKGETAYLPCKFTLSPEDQGPLD---- 54
DB
QY      52 VLVKWLNVQRGS----DPVTIFLRDSSGDHIQAKY---QGRLVHSHK--VPGDVSLOLST 102
      55 --IEWLISPADNQKVDQVILLY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109
DB
QY      103 LEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPT---VTTGSGYGFVTPQG 158
      110 LQLSDIGTYQCKVK-KAPG-----VANKKIHLVVLVKGSGARCYVDG-----EEIG 155
DB
QY      159 MRISLQCCQAR-GSPPISYIWKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAK 214
      156 SDFKICEPKESGLPQYEWQKLSDSQKMPSTWLAEMTSSVISKNASSEYSGTYSCTVR 215
DB
QY      215 GOVGEQHSIDIVKFFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTMDGYLGCT 274
      216 NRVGSDQ-----CLRLNVPPSN-----KA-----GLIAGA 242
DB
QY      275 SAGPGKSLPVFAIILISLCMVFTMAYIMLCRKTSQOEHVYEABARAH 323
      243 IIG---TLALALIGLIIFCC-----RKKRREKEKEKEVHN 275
DB
```

```
RESULT 7
US-09-978-191C-59
; Sequence 59, Application US/09978191C
; GENERAL INFORMATION:
```



```

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191C
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 623
; SEQ ID NO 59
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-978-191C-59

Query Match          7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity 22.2%; Pred. No. 8.3e-06;
Matches 91; Conservative 64; Mismatches 154; Indels 101; Gaps 20,

QY      1  MGILLGLLLGLHL--TVDYTGRRPILLEVPEVSVTGPMKGDVNLPTCYDPLQGYTQVLVKWLV 58
      | :| | | | : : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MSLLLLLLLVSYVGTGLGTHTEIKRAVEAEKVTLPCHHQLGLP-EXDTLD-----IEWLL 53

QY      59 --QRGSDPVTIFLRDSSGDHIQO--AKYQGR-LHVS HKVPGDVSLQLSTLEMDRSHYT 112
      | :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      54 TDNEGNOKVVI---TYSRRHYNNLLTTEEQKGRVAFASNFIAGDASLQIEPLKPSDEGRYT 110

113 CEVTWQTPDGNQVNRDKITELRVQKLSVSKPTVTGSGYGFYTPQGMRIISLQO-ARGSP 171

```

[illegible]

```

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 32378
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (564)..(597)
; OTHER INFORMATION: RECEPTOR INTERLEUKIN-1 PRECURSOR domain identified by
; OTHER INFORMATION: EMATRIX, accession number PD02870B, p-value=7.400e-10, raw score
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (354)..(728)
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,
; OTHER INFORMATION: E-value=1.4e-36, Pfam score of 122.9
US-10-450-763-32378
```

Query Match 7.4%; Score 156; DB 6; Length 737;
Best Local Similarity 24.3%; Pred. No. 3.2e-05;
Matches 73; Conservative 38; Mismatches 128; Indels 62; Gaps 14;

```
QY 4 LLDLLL-----GHLTVDTYGRPI-LEVPESVTGPMKGDVNL 39
DB 465 LLDLKIQTQDLADAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMIGSNVTL 524
QY 40 PCTYDPLQGYTQVLVKWLVRGSDPVTIFLRDSSGDHIQQAQYQRLHSHKVPBGVSLQ 99
DB 525 PCY---VQGYPEPTIKW---RLDNMPIFSRPFSVSSISQLR-TGALFILN----- 568
QY 100 LSTLEMDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVKPTVTGSGYGFVPQGM 159
DB 569 ---LWASDKGTYYICEAENQFGKIQSETTVTVTGLVAPLIGIS-PSVA-----NVI EQ 617
QY 160 RISLQCG-ARGSPPISYIWKQQTN-NOEP-IKVATLSTLLFKPAVIADSGSYFCTAKGQ 216
DB 618 QLTLPCTLLAGNPPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLQDGEYTCVASNV 677
QY 217 VGSEQSDIVKF---VVKDSSKLLKTKTEAPTTMTYPLKATSTVQKS--WDWTTDMDGY 270
DB 678 AGTNKKTTSVVHVLPFIQHGQQLSTIEGIPVTL--PCKASGNPKPSVIMSKVNDTSSY 735
QY 271 L 271
DB 736 I 736
```

RESULT 10
PCT-US05-03880-128
; Sequence 128, Application PC/TUS0503880
; GENERAL INFORMATION:
; APPLICANT: INANA, GEORGE
; APPLICANT: MCLAREN, MARGARET
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL
; FILE REFERENCE: 39532-192229
; CURRENT APPLICATION NUMBER: PCT/US05/03880
; CURRENT FILING DATE: 2005-02-09
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128

LENGTH: 5622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03880-128

Query Match 7.4%; Score 154.5; DB 1; Length 5622;
Best Local Similarity 23.8%; Pred. No. 0.00054;
Matches 93; Conservative 43; Mismatches 152; Indels 103; Gaps 20;

```
QY 4 LLDLLL-----GHLTVDTYGRPI-LEVPESVTGPMKGDVNL 39
DB 753 LLDLKIQTQDLADAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMIGSNVTL 812
QY 40 PCTYDPLQGYTQVLVKWLVRGSDPVTIFLRDSSGDHIQQAQYQRLHSHKVPBGVSLQ 99
DB 813 PCY---VQGYPEPTIKW---RLDNMPIFSRPFSVSSISQLR-TGALFILN----- 856
QY 100 LSTLEMDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVKPTVTGSGYGFVPQGM 159
DB 857 ---LWASDKGTYYICEAENQFGKIQSETTVTVTGLVAPLIGIS-PSVA-----NVI EQ 905
QY 160 RISLQCG-ARGSPPISYIWKQQTN-NOEP-IKVATLSTLLFKPAVIADSGSYFCTAKGQ 216
DB 906 QLTLPCTLLAGNPPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLQDGEYTCVASNV 965
QY 217 VGSEQSDIVKF---VVKDSSKLLKTKTEAPTTMTYPLKATSTVQKSMDWTTDMDGYLG 272
DB 966 AGTNKKTTSVVHVLPFIQHGQQLSTIEGIPVTL--PCKASGNPKPSVIWS--KKGELI 1021
QY 273 ET-----SAGPGKSLPVFAILLIIS-----LCMVVFTMAXIMLCRKTSQGEHYEA 319
DB 1022 STSSAKFSAGADGSL-----YVVSFGGESEGYVCTATNTAGY----AKRKVQLTVY-- 1069
QY 320 ARAHAREANDSGETMRVAIFAS--GCSSDEP 348
DB 1070 -----VRPRVFGDQRLGSLQDKP 1086
```

RESULT 11
US-11-049-637-2
; Sequence 2, Application US/11049637
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: Novel Human Hemiscentin Proteins and Polynucleotides
; FILE REFERENCE: LEX-0235-USA
; CURRENT APPLICATION NUMBER: US/11/049,637
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US/09/953,096
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/232,793
; PRIOR FILING DATE: 2000 09-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5518
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5518)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-049-637-2

Query Match 7.3%; Score 153.5; DB 7; Length 5518;
Best Local Similarity 25.2%; Pred. No. 0.00064;
Matches 80; Conservative 38; Mismatches 132; Indels 67; Gaps 15;
QY 4 LLDLLL-----GHLTVDTYGRPI-LEVPESVTGPMKGDVNL 39
DB 753 LLDLKIQTQDLADAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMIGSNVTL 812

QY	40	PCTYDPLQGYTQVLVKMLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPBGVSLQ	99
Dd	813	PCY---VQGYPEPTIKW---RRLDNMPIFSRXFSVSSISQLR-TGALFILN-----	856
QY	100	LSTLEMDDRSHYTCEVTWTQPDGNQVRDKITELRVQKLVSKEPTVTTSGYGFTVPGCM	159
Dd	857	---LWASDKGTVICEAENQEGKIQSETTVTVTGLVAPLGIS-PSVA-----NVIEGQ	905
QY	160	RISLQCQ-ARGSPPISYIWKQOTN-NQEP-IKVATILSTLLFKPAVIADSGSYFCTAKGQ	216
Dd	906	QLTLPLCTLLAGNPPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVOLQDGGEYTCVASNV	965
QY	217	VGSEQHSDIVKF---VVKDSSKLLKTTEAPTMTYPLKATSTVKQSWDWTDMDYLIG	272
Dd	966	AGTNNTKTSVVVHVHLPTIQHGQOILSTIEGIPVTL-PCKASGNPKPSVIMS--KKGELL	1021
QY	273	ET-----SAGPGKSLPV	284
Dd	1022	STSSAKFSAGADGSLYV	1038

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RESULT 12
; US-10-450-763-32476
; Sequence 32476, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 32476
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (270)..(303)
; OTHER INFORMATION: RECEPTOR INTERLEUKIN-1 PRECURSOR domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD02870B, p-value=7.400e-10, raw score
; OTHER INFORMATION: 18.83
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (60)..(434)
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,
; OTHER INFORMATION: E-value=1.4e-36, Pfam score of 122.9
US-10-450-763-32476

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	Query Match	7.2%;	Score 151;	DB 6;	Length 434;
	Best Local Similarity	24.3%;	Pred. No. 4.3e-05;		
	Matches	71;	Conservative 38;	Mismatches 123;	Indels 60; Gaps 13
Qy	4	LGLLLL-----	-----GHLTVDTYGRPI-LEVPESVTGPWKGDVNL	39	
		:	:: ::: :		
Dd	171	LGLLKIQTODLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPAVDSMEIGSNVTL		230	
Qy	40	PCTYDPLQGYTQVLVKWLVRGSDPVTIFLRDSSGDHIQQAKYQGRLVHSHKVPFGDVSLQ		99	
		:: : :: : : :: :			
Dd	231	PCY---VQGYPEPTIKW--RRLDNMPIFSRPFVSISISQLR-TGALFTLN-----		274	
Qy	100	LSTLEMDDRSHYTCEVTWCOTPDGNQNVVRDKITELRVQKLVSFSKPTVTGGSGYGFTVPQGM		159	
		:: : : : : :: : :: :			
Dd	275	--LWASDKGTYYICEAENQFGKIQSETTVTVTGTGLVAPLIGIS-PSVA-----NVIEWGQ		323	
Qy	160	RISLQCQ-ARGSPPISYIWXQQTN-NQEP-IKVATLSTLLFKPAVIADSGSYECTAKGQ		216	

Db 324 QLTLPCTLLAGNPPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLDGGELTQVASN 383

QY 217 VGSEQHSDIVKF---VVKDSSKLLKTKTEAFTMTYPLKATSTVKQSDMT 264

Db 384 AGTNKTKTSVVVHVLPTIQHGQQLISTIEGIPVTL--PCKASGNPKPSVTS 433

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RESULT 13
US-10-450-763-52760
; Sequence 52760, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450, 763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 52760
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)..(232)
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(361)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52760

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Query Match          7.0%; Score 146.5; DB 6; Length 361;
Best Local Similarity 24.5%; Pred. No. 8.3e-05;
Matches 60; Conservative 31; Mismatches 91; Indels 63; Gaps 11;

QY      9 LIGLITVDTYGR-PILEVPESVTGPMKGDVNLPC-----TYDPLQGTYQLVKMLVQRG 61
       |:|:::||::|| | | | | | :|:|
DB     37 LIGAVNLIKSSNRTPVVGEEFES-----VELSCIITDSQTSDP-----RIEWKKIQD 81
QY      62 SDPVTIFLRDSSGDHIQQAKYQGRLVHSHKVPBGVSLSQLSTLEMDDRSHYTCEVWTQTPTD 121
       :|:|:| | | | | | | | | | | :|:|
DB     82 EQTTYVFEDN-----KIQGDLAGRAEILGKTSLKIMWTRRDSALYRCVVARNND- 131
QY      122 GNQVRDKITELRVOKLSVSKPTVTTGSGYGFTVPQGMKISLQCCAR-GSPPISYIWKQ 180
        |:|:|::|| || | | | | | | | | | |
DB     132 ----RKIEDIAIEVTQVKP-VTPVCRRVPKAVPVGKMATLHCQEGEXGPPPAHYSWYR- 184
QY      181 QTNNGEPIKV-----ATLSTLFKPAVIADSGSYFCTAKGVGS----E 220
        |:|:|:| | | | | | | | | | | |
DB     185 ---NDVPLPTDSRANPRFRNSSFHLNSETGTLVFTA VHKDSDGGYYCIASNDAGSARCEE 241
QY      221 QHSDI 225
       |:::
DB     242 QEMEV 246

RESULT 14
US-10-852-335A-139
; Sequence 139, Application US/10852335A
; GENERAL INFORMATION:
; APPLICANT: HEIDI S. PHILLIPS
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumors of Glial Origin
; FILE REFERENCE: P5103R1-US
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 15:09:10 ; Search time 24 Seconds
(without alignments)
1241.041 Million cell updates/sec

Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILLGLLLGHLTYDTYGR.....LDDTVPLDYFLATEGKSVK 399

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	80.5	321	4	US-09-254-465A-2 Sequence 2, Appli
2	1688	80.5	321	4	US-09-953-499-2 Sequence 2, Appli
3	1547	73.7	306	4	US-09-369-247-63 Sequence 63, Appli
4	870	41.5	175	4	US-09-763-902B-6 Sequence 6, Appli
5	178.5	8.5	299	3	US-09-188-930-189 Sequence 189, App
6	178.5	8.5	299	3	US-09-188-930-331 Sequence 331, App
7	178.5	8.5	299	3	US-09-462-270-2 Sequence 2, Appli
8	178.5	8.5	299	4	US-09-254-465A-1 Sequence 1, Appli
9	178.5	8.5	299	4	US-09-312-283C-189 Sequence 189, App
10	178.5	8.5	299	4	US-09-312-283C-331 Sequence 331, App
11	178.5	8.5	299	4	US-09-907-794A-119 Sequence 119, App
12	178.5	8.5	299	4	US-09-905-125A-119 Sequence 119, App
13	178.5	8.5	299	4	US-09-902-775A-119 Sequence 119, App
14	178.5	8.5	299	4	US-09-397-243D-3 Sequence 3, Appli
15	178.5	8.5	299	4	US-09-906-700-119 Sequence 119, App
16	178.5	8.5	299	4	US-09-903-603A-119 Sequence 119, App
17	178.5	8.5	299	4	US-09-904-920A-119 Sequence 119, App
18	178.5	8.5	299	4	US-09-909-064-119 Sequence 119, App
19	178.5	8.5	299	4	US-09-905-381A-119 Sequence 119, App
20	178.5	8.5	299	4	US-09-906-618-119 Sequence 119, App
21	178.5	8.5	299	4	US-09-953-499-1 Sequence 1, Appli
22	177	8.4	319	1	US-08-597-495B-22 Sequence 22, Appli
23	177	8.4	319	3	US-09-068-051A-22 Sequence 22, Appli
24	177	8.4	319	4	US-09-336-536-67 Sequence 67, Appli
25	177	8.4	319	4	US-09-254-465A-6 Sequence 6, Appli
26	177	8.4	319	4	US-09-953-499-6 Sequence 6, Appli
27	176	8.4	270	4	US-09-254-465A-24 Sequence 24, Appli

28	176	8.4	270	4	US-09-953-499-24	Sequence 24, Appli
29	176	8.4	273	4	US-09-254-465A-26	Sequence 26, Appli
30	176	8.4	273	4	US-09-953-499-26	Sequence 26, Appli
31	172.5	8.2	316	4	US-09-397-243D-13	Sequence 13, Appli
32	169.5	8.1	260	4	US-09-254-465A-23	Sequence 23, Appli
33	169.5	8.1	260	4	US-09-953-499-23	Sequence 23, Appli
34	169.5	8.1	263	4	US-09-254-465A-25	Sequence 25, Appli
35	169.5	8.1	263	4	US-09-953-499-25	Sequence 25, Appli
36	167	8.0	300	4	US-09-254-465A-10	Sequence 10, Appli
37	167	8.0	300	4	US-09-397-243D-12	Sequence 12, Appli
38	167	8.0	300	4	US-09-953-499-10	Sequence 10, Appli
39	167	8.0	365	4	US-09-899-634C-4	Sequence 4, Appli
40	163.5	7.8	261	4	US-09-899-634C-2	Sequence 2, Appli
41	163	7.8	318	3	US-09-068-051A-32	Sequence 32, Appli
42	159	7.6	365	2	US-08-979-424-3	Sequence 3, Appli
43	159	7.6	365	3	US-08-928-383B-2	Sequence 2, Appli
44	159	7.6	365	3	US-09-272-496-2	Sequence 2, Appli
45	159	7.6	365	4	US-09-949-016-6064	Sequence 6064, Ap
46	159	7.6	383	4	US-09-949-016-11050	Sequence 11050, A
47	151	7.2	466	4	US-09-604-107A-8	Sequence 8, Appli
48	150	7.1	1395	3	US-09-540-245A-15	Sequence 15, Appli
49	142.5	6.8	398	4	US-09-778-510-4	Sequence 4, Appli
50	142.5	6.8	894	4	US-09-949-016-10605	Sequence 10605, A
51	140.5	6.7	365	3	US-08-928-383B-23	Sequence 23, Appli
52	140.5	6.7	365	3	US-08-928-383B-24	Sequence 24, Appli
53	140.5	6.7	365	3	US-08-928-383B-26	Sequence 26, Appli
54	139	6.6	561	4	US-09-866-510-24	Sequence 24, Appli
55	139	6.6	1090	4	US-09-866-510-14	Sequence 14, Appli
56	139	6.6	1106	1	US-08-180-195-2	Sequence 2, Appli
57	139	6.6	1106	1	US-08-168-917-2	Sequence 2, Appli
58	139	6.6	1106	1	US-08-477-329-2	Sequence 2, Appli
59	139	6.6	1106	2	US-08-475-458-2	Sequence 2, Appli
60	139	6.6	1106	2	US-08-460-510-2	Sequence 2, Appli
61	139	6.6	1106	2	US-08-460-490-2	Sequence 2, Appli
62	139	6.6	1106	3	US-08-980-400-2	Sequence 2, Appli
63	139	6.6	1106	3	US-08-462-728-4	Sequence 4, Appli
64	139	6.6	1106	3	US-09-583-459A-2	Sequence 2, Appli
65	139	6.6	1106	3	US-09-583-210-2	Sequence 2, Appli
66	139	6.6	1106	3	US-09-583-449A-2	Sequence 2, Appli
67	139	6.6	1106	3	US-09-435-059-2	Sequence 2, Appli
68	139	6.6	1106	3	US-08-461-917-4	Sequence 4, Appli
69	139	6.6	1106	4	US-08-464-436-4	Sequence 4, Appli
70	139	6.6	1106	4	US-08-464-436-4	Sequence 4, Appli
71	139	6.6	1106	4	US-09-866-510-16	Sequence 16, Appli
72	139	6.6	1106	4	US-09-866-510-18	Sequence 18, Appli
73	139	6.6	1106	4	US-09-866-510-20	Sequence 20, Appli
74	139	6.6	1106	4	US-09-866-510-22	Sequence 22, Appli
75	139	6.6	1106	5	PCT-US92-00730-2	Sequence 2, Appli
76	139	6.6	1106	5	PCT-US92-00862-2	Sequence 2, Appli
77	138.5	6.6	310	4	US-09-907-794A-423	Sequence 423, App
78	138.5	6.6	310	4	US-09-905-125A-423	Sequence 423, App
79	138.5	6.6	310	4	US-09-902-775A-423	Sequence 423, App
80	138.5	6.6	310	4	US-09-906-700-423	Sequence 423, App
81	138.5	6.6	310	4	US-09-903-603A-423	Sequence 423, App
82	138.5	6.6	310	4	US-09-904-920A-423	Sequence 423, App
83	138.5	6.6	310	4	US-09-909-064-423	Sequence 423, App
84	138.5	6.6	310	4	US-09-905-381A-423	Sequence 423, App
85	138.5	6.6	310	4	US-09-906-618-423	Sequence 423, App
86	138	6.6	360	4	US-09-907-794A-213	Sequence 213, App
87	138	6.6	360	4	US-09-905-125A-213	Sequence 213, App
88	138	6.6	360	4	US-09-902-775A-213	Sequence 213, App
89	138	6.6	360	4	US-09-906-700-213	Sequence 213, App
90	138	6.6	360	4	US-09-903-603A-213	Sequence 213, App
91	138	6.6	360	4	US-09-904-920A-213	Sequence 213, App
92	138	6.6	360	4	US-09-909-064-213	Sequence 213, App
93	138	6.6	360	4	US-09-905-381A-213	Sequence 213, App
94	138	6.6	360	4	US-09-906-618-213	Sequence 213, App
95	138	6.6	1059	4	US-09-907-794A-290	Sequence 290, App
96	138	6.6	1059	4	US-09-905-125A-290	Sequence 290, App
97	138	6.6	1059	4	US-09-902-775A-290	Sequence 290, App
98	138	6.6	1059	4	US-09-906-700-290	Sequence 290, App
99	138	6.6	1059	4	US-09-903-603A-290	Sequence 290, App
100	138	6.6	1059	4	US-09-904-920A-290	Sequence 290, App

101	138	6.6	1059	4	US-09-909-064-290	Sequence 290, App
102	138	6.6	1059	4	US-09-905-381A-290	Sequence 290, App
103	138	6.6	1059	4	US-09-906-618-290	Sequence 290, App
104	138	6.6	1119	4	US-09-907-794A-294	Sequence 294, App
105	138	6.6	1119	4	US-09-905-125A-294	Sequence 294, App
106	138	6.6	1119	4	US-09-902-775A-294	Sequence 294, App
107	138	6.6	1119	4	US-09-906-700-294	Sequence 294, App
108	138	6.6	1119	4	US-09-903-603A-294	Sequence 294, App
109	138	6.6	1119	4	US-09-904-920A-294	Sequence 294, App
110	138	6.6	1119	4	US-09-909-064-294	Sequence 294, App
111	138	6.6	1119	4	US-09-905-381A-294	Sequence 294, App
112	138	6.6	1119	4	US-09-906-618-294	Sequence 294, App
113	137	6.5	398	4	US-09-778-510-6	Sequence 6, Appli
114	137	6.5	398	4	US-09-907-794A-84	Sequence 84, Appl
115	137	6.5	398	4	US-09-905-125A-84	Sequence 84, Appl
116	137	6.5	398	4	US-09-902-775A-84	Sequence 84, Appl
117	137	6.5	398	4	US-09-906-700-84	Sequence 84, Appl
118	137	6.5	398	4	US-09-903-603A-84	Sequence 84, Appl
119	137	6.5	398	4	US-09-904-920A-84	Sequence 84, Appl
120	137	6.5	398	4	US-09-909-064-84	Sequence 84, Appl
121	137	6.5	398	4	US-09-905-381A-84	Sequence 84, Appl
122	137	6.5	398	4	US-09-906-618-84	Sequence 84, Appl
123	137	6.5	432	4	US-09-778-510-2	Sequence 2, Appli
124	137	6.5	450	4	US-09-907-794A-320	Sequence 320, App
125	137	6.5	450	4	US-09-905-125A-320	Sequence 320, App
126	137	6.5	450	4	US-09-902-775A-320	Sequence 320, App
127	137	6.5	450	4	US-09-906-700-320	Sequence 320, App
128	137	6.5	450	4	US-09-903-603A-320	Sequence 320, App
129	137	6.5	450	4	US-09-904-920A-320	Sequence 320, App
130	137	6.5	450	4	US-09-909-064-320	Sequence 320, App
131	137	6.5	450	4	US-09-905-381A-320	Sequence 320, App
132	137	6.5	450	4	US-09-906-618-320	Sequence 320, App
133	136	6.5	205	3	US-09-462-270-4	Sequence 4, Appli
134	135	6.4	294	4	US-09-336-536-42	Sequence 42, Appl
135	135	6.4	394	4	US-09-336-536-39	Sequence 39, Appl
136	134.5	6.4	193	4	US-09-397-243D-4	Sequence 4, Appli
137	134.5	6.4	440	3	US-08-759-628-4	Sequence 4, Appli
138	134	6.4	440	4	US-09-866-028-61	Sequence 61, Appl
139	134	6.4	440	4	US-09-944-457-61	Sequence 61, Appl
140	134	6.4	442	4	US-09-778-510-20	Sequence 20, Appl
141	134	6.4	442	4	US-09-930-803-1	Sequence 1, Appli
142	133.5	6.4	467	3	US-09-046-736-2	Sequence 2, Appli
143	132.5	6.3	630	2	US-08-752-307B-14	Sequence 14, Appl
144	132.5	6.3	630	3	US-09-707-802-14	Sequence 14, Appl
145	132.5	6.3	630	3	US-09-991-326-14	Sequence 14, Appl
146	131	6.2	4391	4	US-10-006-011A-2	Sequence 2, Appli
147	130	6.2	624	4	US-08-467-602-325	Sequence 326, App
148	130	6.2	624	4	US-08-411-295F-252	Sequence 352, App
149	130	6.2	658	4	US-08-467-602-368	Sequence 368, App
150	130	6.2	658	4	US-08-411-295F-294	Sequence 294, App
151	130	6.2	841	4	US-08-467-602-327	Sequence 327, App
152	130	6.2	841	4	US-08-411-295F-253	Sequence 253, App
153	130	6.2	875	4	US-08-467-602-369	Sequence 369, App
154	130	6.2	875	4	US-08-411-295F-295	Sequence 295, App
155	130	6.2	888	4	US-08-467-602-325	Sequence 325, App
156	130	6.2	888	4	US-08-411-295F-251	Sequence 251, App
157	130	6.2	922	4	US-08-467-602-367	Sequence 367, App
158	130	6.2	922	4	US-08-411-295F-293	Sequence 293, App
159	129.5	6.2	315	4	US-09-910-174B-28	Sequence 28, Appl
160	129.5	6.2	315	4	US-09-620-461-28	Sequence 28, Appl
161	129	6.1	303	4	US-09-651-200-23	Sequence 23, Appl
162	129	6.1	303	4	US-09-441-411-15	Sequence 15, Appl
163	129	6.1	303	4	US-09-441-411-20	Sequence 20, Appl
164	129	6.1	309	2	US-08-456-104-4	Sequence 4, Appli
165	129	6.1	309	3	US-08-479-744A-23	Sequence 23, Appl
166	129	6.1	309	3	US-08-280-757B-23	Sequence 21, Appl
167	129	6.1	309	3	US-08-205-697A-21	Sequence 21, Appl
168	129	6.1	309	3	US-08-702-525-21	Sequence 22, Appl
169	129	6.1	309	4	US-09-651-200-22	Sequence 22, Appl
170	129	6.1	309	4	US-09-667-135-33	Sequence 33, Appl
171	129	6.1	309	4	US-09-425-762-23	Sequence 23, Appl
172	129	6.1	309	4	US-09-837-867A-21	Sequence 21, Appl
173	129	6.1	309	4	US-09-206-132-4	Sequence 4, Appli
174	129	6.1	309	4	US-09-441-411-13	Sequence 13, Appl
175	129	6.1	309	4	US-09-441-411-18	Sequence 18, Appl
176	129	6.1	309	4	US-09-441-411-24	Sequence 24, Appl
177	129	6.1	309	4	US-09-425-516-23	Sequence 23, Appl
178	129	6.1	309	5	PCT-US95-02576-21	Sequence 21, Appl
179	129	6.1	314	3	US-08-205-697A-13	Sequence 13, Appl
180	129	6.1	314	3	US-08-702-525-13	Sequence 13, Appl
181	129	6.1	314	4	US-09-837-867A-13	Sequence 14, Appl
182	129	6.1	314	4	US-09-441-411-14	Sequence 14, Appl
183	129	6.1	314	4	US-09-441-411-19	Sequence 19, Appl
184	129	6.1	314	5	PCT-US95-02576-13	Sequence 13, Appl
185	129	6.1	356	4	US-09-441-411-11	Sequence 11, Appl
186	129	6.1	356	4	US-09-441-411-12	Sequence 12, Appl
187	129	6.1	356	4	US-09-441-411-16	Sequence 16, Appl
188	129	6.1	356	4	US-09-441-411-17	Sequence 17, Appl
189	129	6.1	1248	4	US-09-949-016-10595	Sequence 10595, A
190	129	6.1	1248	4	US-09-949-016-10596	Sequence 10596, A
191	128.5	6.1	613	3	US-08-470-335-230	Sequence 230, App
192	128.5	6.1	613	4	US-08-467-602-329	Sequence 329, App
193	128.5	6.1	613	4	US-08-411-295F-255	Sequence 255, App
194	128.5	6.1	633	4	US-08-467-602-335	Sequence 335, App
195	128.5	6.1	633	4	US-08-411-295F-261	Sequence 261, App
196	128.5	6.1	647	4	US-08-467-602-371	Sequence 371, App
197	128.5	6.1	647	4	US-08-411-295F-297	Sequence 297, App
198	128.5	6.1	667	4	US-08-467-602-377	Sequence 377, App
199	128.5	6.1	667	4	US-08-411-295F-303	Sequence 303, App
200	128.5	6.1	830	3	US-08-470-335-231	Sequence 231, App
201	128.5	6.1	830	4	US-08-467-602-330	Sequence 330, App
202	128.5	6.1	830	4	US-08-411-295F-256	Sequence 256, App
203	128.5	6.1	850	4	US-08-467-602-336	Sequence 336, App
204	128.5	6.1	850	4	US-08-411-295F-262	Sequence 262, App
205	128.5	6.1	864	4	US-08-467-602-372	Sequence 372, App
206	128.5	6.1	864	4	US-08-470-335-232	Sequence 232, App
207	128.5	6.1	877	3	US-08-470-335-232	Sequence 232, App
208	128.5	6.1	877	4	US-08-467-602-331	Sequence 331, App
209	128.5	6.1	877	4	US-08-411-295F-257	Sequence 257, App
210	128.5	6.1	884	4	US-08-467-602-378	Sequence 378, App
211	128.5	6.1	884	4	US-08-411-295F-304	Sequence 304, App
212	128.5	6.1	897	4	US-08-467-602-337	Sequence 337, App
213	128.5	6.1	897	4	US-08-411-295F-263	Sequence 263, App
214	128.5	6.1	911	4	US-08-467-602-373	Sequence 373, App
215	128.5	6.1	911	4	US-08-411-295F-299	Sequence 299, App
216	128.5	6.1	931	4	US-08-467-602-379	Sequence 379, App
217	128.5	6.1	931	4	US-08-411-295F-305	Sequence 305, App
218	128	6.1	423	4	US-09-778-510-22	Sequence 22, Appl
219	128	6.1	479	4	US-09-723-368-2	Sequence 2, Appli
220	128	6.1	479	4	US-09-949-016-6278	Sequence 6278, Ap
221	128	6.1	522	4	US-09-949-016-7563	Sequence 7563, Ap
222	127	6.1	227	4	US-09-205-258-947	Sequence 947, App
223	127	6.1	462	2	US-08-752-307B-7	Sequence 7, Appli
224	127	6.1	462	3	US-09-707-802-7	Sequence 7, Appli
225	127	6.1	462	3	US-09-991-326-7	Sequence 7, Appli
226	127	6.1	465	2	US-08-752-307B-5	Sequence 5, Appli
227	127	6.1	465	3	US-09-707-802-5	Sequence 5, Appli
228	127	6.1	465	3	US-09-991-326-5	Sequence 5, Appli
229	126.5	6.0	924	1	US-08-481-130-28	Sequence 28, Appl
230	126.5	6.0	924	1	US-08-485-984A-28	Sequence 28, Appl
231	126.5	6.0	924	1	US-08-487-595-28	Sequence 28, Appl
232	126.5	6.0	924	2	US-08-175-928-2	Sequence 2, Appli
233	124.5	5.9	387	3	US-09-175-928-2	Sequence 2, Appli
234	123.5	5.9	833	4	US-09-949-016-11496	Sequence 11496, A
235	123.5	5.9	1180	4	US-09-949-016-6577	Sequence 6577, Ap
236	123	5.9	313	4	US-09-700-397-4	Sequence 4, Appli
237	123	5.9	344	4	US-09-700-397-3	Sequence 3, Appli
238	123	5.9	464	2	US-08-602-725-32	Sequence 32, Appl
239	123	5.9	464	4	US-09-949-016-7525	Sequence 7525, Ap
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243	122.5	5.8	612	3	US-09-707-802-11	Sequence 11, Appl
244	122.5	5.8	612	3	US-09-991-326-11	Sequence 32, Appl
245	122.5	5.8	738	3	US-08-478-208-32	Sequence 32, Appl
246	122.5	5.8	738	4	US-09-336-536-73	Sequence 73, Appl

393	117	5.6	292	4	US-09-800-729-175	Sequence 175, App	466	115.5	5.5	738	6	5264554-2	Patent No. 5264554
394	117	5.6	409	4	US-08-467-602-284	Sequence 284, App	467	115.5	5.5	1253	3	US-08-506-296B-14	Sequence 14, Appl
395	117	5.6	406	4	US-08-411-295F-210	Sequence 210, App	468	115	5.5	668	4	US-09-949-016-8139	Sequence 8139, Ap
396	117	5.6	626	4	US-08-467-602-285	Sequence 285, App	469	115	5.5	819	4	US-09-949-016-11044	Sequence 11044, A
397	117	5.6	626	4	US-08-411-295F-211	Sequence 211, App	470	115	5.5	1209	4	US-09-130-158A-2	Sequence 2, Appli
398	117	5.6	638	3	US-08-470-335-240	Sequence 240, App	471	114.5	5.5	421	2	US-08-659-984A-1	Sequence 1, Appli
399	117	5.6	638	4	US-08-467-602-297	Sequence 297, App	472	114.5	5.5	421	3	US-08-660-531-1	Sequence 1, Appli
400	117	5.6	638	4	US-08-411-295F-223	Sequence 223, App	473	114.5	5.5	422	3	US-08-753-007A-9	Sequence 9, Appli
401	117	5.6	650	3	US-09-310-463-2	Sequence 2, Appli	474	114.5	5.5	422	3	US-09-398-496-9	Sequence 9, Appli
402	117	5.6	650	4	US-08-842-248A-2	Sequence 2, Appli	475	114.5	5.5	444	2	US-08-659-984A-5	Sequence 5, Appli
403	117	5.6	651	3	US-08-985-950-22	Sequence 22, Appl	476	114.5	5.5	444	3	US-08-660-531-5	Sequence 5, Appli
404	117	5.6	651	4	US-09-546-049-22	Sequence 22, Appl	477	114.5	5.5	504	4	US-09-949-016-7020	Sequence 7020, Ap
405	117	5.6	672	4	US-08-467-602-339	Sequence 339, App	478	114.5	5.5	511	4	US-09-949-016-11380	Sequence 11380, A
406	117	5.6	672	4	US-08-411-295F-265	Sequence 265, App	479	114.5	5.5	514	4	US-09-949-016-11380	Sequence 11380, A
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408	117	5.6	853	4	US-08-411-295F-209	Sequence 209, App	481	114.5	5.5	917	1	US-08-245-295-2	Sequence 2, Appli
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410	117	5.6	855	4	US-08-467-602-298	Sequence 298, App	483	114.5	5.5	917	1	US-08-656-984A-2	Sequence 2, Appli
411	117	5.6	855	4	US-08-411-295F-224	Sequence 224, App	484	114.5	5.5	917	1	US-08-485-604-2	Sequence 2, Appli
412	117	5.6	889	4	US-08-467-602-340	Sequence 340, App	485	114.5	5.5	917	2	US-08-487-595-2	Sequence 2, Appli
413	117	5.6	889	4	US-08-411-295F-266	Sequence 266, App	486	114	5.4	364	4	US-08-467-602-245	Sequence 245, App
414	117	5.6	902	3	US-08-470-335-242	Sequence 242, App	487	114	5.4	364	4	US-08-411-295F-171	Sequence 171, App
415	117	5.6	902	4	US-08-467-602-296	Sequence 296, App	488	114	5.4	384	4	US-08-467-602-251	Sequence 251, App
416	117	5.6	902	4	US-08-411-295F-222	Sequence 222, App	489	114	5.4	384	4	US-08-411-295F-177	Sequence 177, App
417	117	5.6	936	4	US-08-467-602-338	Sequence 338, App	490	114	5.4	581	4	US-08-467-602-246	Sequence 246, App
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419	117	5.6	1447	3	US-09-041-886-25	Sequence 25, Appl	492	114	5.4	601	4	US-08-467-602-252	Sequence 252, App
420	117	5.6	1447	5	PCT-US94-05277-2	Sequence 2, Appli	493	114	5.4	601	4	US-08-411-295F-178	Sequence 178, App
421	117	5.6	1745	4	US-09-800-729-89	Sequence 89, Appl	494	114	5.4	602	1	US-08-428-926-5	Sequence 5, Appli
422	116.5	5.6	315	2	US-08-414-657D-47	Sequence 47, Appl	495	114	5.4	602	1	US-08-428-927-5	Sequence 5, Appli
423	116.5	5.6	338	2	US-08-414-657D-42	Sequence 42, Appl	496	114	5.4	602	1	US-08-428-298-5	Sequence 5, Appli
424	116.5	5.6	338	2	US-08-414-657D-43	Sequence 43, Appl	497	114	5.4	602	1	US-08-339-517-5	Sequence 5, Appli
425	116.5	5.6	338	4	US-09-135-080-4	Sequence 4, Appli	498	114	5.4	628	4	US-08-467-602-247	Sequence 247, App
426	116.5	5.6	607	2	US-08-752-307B-12	Sequence 12, Appl	499	114	5.4	628	4	US-08-411-295F-173	Sequence 173, App
427	116.5	5.6	607	3	US-09-707-802-12	Sequence 12, Appl	500	114	5.4	648	4	US-08-467-602-253	Sequence 253, App
428	116.5	5.6	607	3	US-09-991-326-12	Sequence 12, Appl	501	114	5.4	648	4	US-08-411-295F-179	Sequence 179, App
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432	116	5.5	610	4	US-08-467-602-332	Sequence 332, App	505	113.5	5.4	534	4	US-09-651-200-6	Sequence 6, Appli
433	116	5.5	610	4	US-08-411-295F-258	Sequence 258, App	506	113.5	5.4	534	4	US-09-651-200-24	Sequence 24, Appl
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435	116	5.5	644	4	US-08-411-295F-300	Sequence 300, App	508	113.5	5.4	601	4	US-08-467-602-323	Sequence 323, App
436	116	5.5	827	3	US-08-470-335-237	Sequence 237, App	509	113.5	5.4	601	4	US-08-411-295F-249	Sequence 249, App
437	116	5.5	827	4	US-08-467-602-333	Sequence 333, App	510	113.5	5.4	635	4	US-08-467-602-365	Sequence 365, App
438	116	5.5	827	4	US-08-411-295F-259	Sequence 259, App	511	113.5	5.4	635	4	US-08-411-295F-291	Sequence 291, App
439	116	5.5	861	4	US-08-467-602-375	Sequence 375, App	512	113.5	5.4	818	3	US-08-470-335-234	Sequence 234, App
440	116	5.5	861	4	US-08-411-295F-301	Sequence 301, App	513	113.5	5.4	818	4	US-08-467-602-321	Sequence 321, App
441	116	5.5	874	3	US-08-470-335-238	Sequence 238, App	514	113.5	5.4	818	4	US-08-411-295F-247	Sequence 247, App
442	116	5.5	874	4	US-08-467-602-334	Sequence 334, App	515	113.5	5.4	852	4	US-08-467-602-363	Sequence 363, App
443	116	5.5	874	4	US-08-411-295F-260	Sequence 260, App	516	113.5	5.4	852	4	US-08-411-295F-289	Sequence 289, App
444	116	5.5	908	4	US-08-467-602-376	Sequence 376, App	517	113.5	5.4	865	3	US-08-470-335-235	Sequence 235, App
445	116	5.5	908	4	US-08-411-295F-302	Sequence 302, App	518	113.5	5.4	865	4	US-08-467-602-322	Sequence 322, App
446	116	5.5	1709	4	US-09-949-016-10503	Sequence 10503, A	519	113.5	5.4	865	4	US-08-411-295F-248	Sequence 248, App
447	115.5	5.5	375	4	US-08-467-602-242	Sequence 242, App	520	113.5	5.4	899	4	US-08-467-602-364	Sequence 364, App
448	115.5	5.5	375	4	US-08-411-295F-168	Sequence 168, App	521	113.5	5.4	899	4	US-08-467-602-364	Sequence 290, App
449	115.5	5.5	398	4	US-08-467-602-287	Sequence 287, App	522	113	5.4	287	2	US-08-414-657D-48	Sequence 48, Appl
450	115.5	5.5	398	4	US-08-411-295F-213	Sequence 213, App	523	113	5.4	294	6	5260223-1	Patent No. 5260223
451	115.5	5.5	418	4	US-08-467-602-293	Sequence 293, App	524	113	5.4	294	6	5260223-1	Patent No. 5260223
452	115.5	5.5	418	4	US-08-411-295F-219	Sequence 219, App	525	113	5.4	304	2	US-08-414-657D-44	Sequence 44, Appl
453	115.5	5.5	592	4	US-08-467-602-243	Sequence 243, App	526	113	5.4	497	4	US-09-499-846-6	Sequence 6, Appli
454	115.5	5.5	592	4	US-08-411-295F-169	Sequence 169, App	527	113	5.4	497	4	US-09-499-846-10	Sequence 10, Appli
455	115.5	5.5	615	4	US-08-467-602-288	Sequence 288, App	528	113	5.4	602	1	US-08-168-091A-2	Sequence 2, Appli
456	115.5	5.5	615	4	US-08-411-295F-214	Sequence 214, App	529	112.5	5.4	389	4	US-08-467-602-213	Sequence 213, App
457	115.5	5.5	635	4	US-08-467-602-294	Sequence 294, App	530	112.5	5.4	389	4	US-08-411-295F-139	Sequence 139, App
458	115.5	5.5	635	4	US-08-411-295F-220	Sequence 220, App	531	112.5	5.4	423	4	US-08-467-602-255	Sequence 255, App
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462	115.5	5.5	662	4	US-08-411-295F-215	Sequence 215, App	535	112.5	5.4	606	4	US-08-411-295F-140	Sequence 140, App
463	115.5	5.5	682	4	US-08-467-602-295	Sequence 295, App	536	112.5	5.4	625	1	US-07-847-743B-26	Sequence 26, Appl
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465	115.5	5.5	738	6	5264554-2	Patent No. 5264554	538	112.5	5.4	625	2	US-08-456-241-26	Sequence 26, Appl

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541	112.5	5.4	640	4	US-08-411-295F-182	Sequence 182, App
542	112.5	5.4	653	4	US-08-467-602-212	Sequence 212, App
543	112.5	5.4	653	4	US-08-411-295F-138	Sequence 138, App
544	112.5	5.4	669	1	US-07-847-743B-8	Sequence 8, Appl1
545	112.5	5.4	669	1	US-07-847-743B-13	Sequence 13, Appl
546	112.5	5.4	669	1	US-08-456-201-8	Sequence 8, Appl1
547	112.5	5.4	669	1	US-08-456-201-13	Sequence 13, Appl1
548	112.5	5.4	669	2	US-08-330-161-11	Sequence 11, Appl
549	112.5	5.4	669	2	US-08-456-241-8	Sequence 8, Appl1
550	112.5	5.4	669	2	US-08-456-241-13	Sequence 13, Appl
551	112.5	5.4	669	2	US-08-440-401-11	Sequence 11, Appl
552	112.5	5.4	669	2	US-08-419-878B-11	Sequence 11, Appl
553	112.5	5.4	669	3	US-09-173-480-11	Sequence 11, Appl
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555	112.5	5.4	669	5	PCT-US92-04295A-13	Sequence 13, Appl
556	112.5	5.4	687	4	US-08-467-602-254	Sequence 254, App
557	112.5	5.4	687	4	US-08-411-295F-180	Sequence 180, App
558	112	5.3	287	2	US-08-414-657D-49	Sequence 49, Appl
559	112	5.3	310	2	US-08-414-657D-45	Sequence 45, Appl
560	112	5.3	322	3	US-09-383-586-33	Sequence 33, Appl
561	112	5.3	322	4	US-09-823-038A-33	Sequence 33, Appl
562	112	5.3	374	3	US-09-046-736-4	Sequence 4, Appl1
563	112	5.3	946	5	PCT-US95-08493-13	Sequence 13, Appl
564	112	5.3	1070	4	US-09-961-403-3	Sequence 3, Appl1
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568	111.5	5.3	869	2	US-08-644-271-29	Sequence 29, Appl
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571	111	5.3	252	2	US-08-414-657D-57	Sequence 57, Appl
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575	110.5	5.3	390	4	US-09-907-794A-39	Sequence 39, Appl
576	110.5	5.3	390	4	US-09-905-125A-39	Sequence 39, Appl
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581	110.5	5.3	390	4	US-09-909-064-39	Sequence 39, Appl
582	110.5	5.3	390	4	US-09-905-381A-39	Sequence 39, Appl
583	110.5	5.3	390	4	US-09-906-618-39	Sequence 39, Appl
584	110.5	5.3	513	4	US-09-910-174B-18	Sequence 18, Appl
585	110.5	5.3	513	4	US-09-620-461-18	Sequence 18, Appl
586	110.5	5.3	635	3	US-08-470-335-247	Sequence 247, App
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588	110.5	5.3	635	4	US-08-411-295F-228	Sequence 228, App
589	110.5	5.3	669	4	US-08-467-602-344	Sequence 344, App
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596	110.5	5.3	899	3	US-08-470-335-249	Sequence 249, App
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607	110	5.2	547	2	US-08-483-389-1	Sequence 1, Appl1
608	110	5.2	547	2	US-08-487-113D-1	Sequence 1, Appl1
609	110	5.2	547	2	US-08-473-503-1	Sequence 1, Appl1
610	110	5.2	547	2	US-08-483-932-1	Sequence 1, Appl1
611	110	5.2	547	2	US-08-720-420A-1	Sequence 1, Appl1
612	110	5.2	547	3	US-08-714-017-1	Sequence 1, Appl1
613	110	5.2	547	3	US-08-863-790-1	Sequence 1, Appl1
614	110	5.2	547	3	US-08-475-680-1	Sequence 1, Appl1
615	110	5.2	547	3	US-08-296-749-1	Sequence 1, Appl1
616	110	5.2	547	4	US-08-314-369-1	Sequence 1, Appl1
617	110	5.2	558	4	US-09-667-135-31	Sequence 31, Appl
618	110	5.2	837	4	US-09-949-016-6515	Sequence 6515, App
619	109.5	5.2	307	4	US-09-197-970B-3	Sequence 3, Appl1
620	109.5	5.2	488	4	US-09-499-846-12	Sequence 12, Appl
621	109.5	5.2	526	4	US-09-910-174B-9	Sequence 9, Appl1
622	109.5	5.2	526	4	US-09-620-461-9	Sequence 9, Appl1
623	109.5	5.2	526	4	US-09-949-016-6122	Sequence 6122, App
624	109.5	5.2	339	4	US-09-949-016-11644	Sequence 11644, A
625	109	5.2	339	4	US-09-719-243-2	Sequence 2, Appl1
626	109	5.2	358	4	US-09-719-243-3	Sequence 3, Appl1
627	109	5.2	389	4	US-08-467-602-276	Sequence 276, App
628	109	5.2	389	4	US-08-411-295F-202	Sequence 202, App
629	109	5.2	486	2	US-08-432-016-6	Sequence 6, Appl1
630	109	5.2	486	2	US-08-684-594-6	Sequence 6, Appl1
631	109	5.2	525	4	US-09-499-846-4	Sequence 4, Appl1
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633	109	5.2	525	4	US-08-467-602-277	Sequence 277, App
634	109	5.2	606	4	US-08-411-295F-203	Sequence 203, App
635	109	5.2	622	4	US-09-499-846-2	Sequence 2, Appl1
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637	109	5.2	646	4	US-09-949-016-6728	Sequence 6728, App
638	109	5.2	646	4	US-09-653-961-2	Sequence 2, Appl1
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646	108	5.1	644	3	US-08-470-335-250	Sequence 250, App
647	108	5.1	644	4	US-08-467-602-311	Sequence 311, App
648	108	5.1	644	4	US-08-411-295F-237	Sequence 237, App
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650	108	5.1	678	4	US-08-411-295F-279	Sequence 279, App
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659	108	5.1	895	4	US-08-411-295F-280	Sequence 280, App
660	108	5.1	908	3	US-08-470-335-252	Sequence 252, App
661	108	5.1	908	4	US-08-467-602-313	Sequence 313, App
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664	108	5.1	942	4	US-08-411-295F-281	Sequence 281, App
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671	107.5	5.1	355	4	US-08-411-295F-160	Sequence 160, App
672	107.5	5.1	572	4	US-08-467-602-235	Sequence 235, App
673	107.5	5.1	572	4	US-08-411-295F-161	Sequence 161, App
674	107.5	5.1	619	4	US-08-467-602-233	Sequence 233, App
675	107.5	5.1	619	4	US-08-411-295F-159	Sequence 159, App
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677	107.5	5.1	731	1	US-08-441-944A-5	Sequence 5, Appl1
678	107.5	5.1	731	1	US-08-439-992A-3	Sequence 3, Appl1
679	107.5	5.1	1297	3	US-08-540-245A-17	Sequence 17, Appl
680	107.5	5.1	1311	1	US-08-340-011-5	Sequence 5, Appl1
681	107.5	5.1	1311	3	US-08-901-710-5	Sequence 5, Appl1
682	107.5	5.1	1311	4	US-09-169-079-5	Sequence 5, Appl1
683	107	5.1	624	2	US-08-642-406A-22	Sequence 22, Appl
684	107	5.1	624	3	US-09-199-534-22	Sequence 22, Appl

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686	107	5.1	729	1	US-07-640-029-3	Sequence 3, Appli
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689	106.5	5.1	395	4	US-08-411-295F-153	Sequence 153, App
690	106.5	5.1	429	4	US-08-467-602-269	Sequence 269, App
691	106.5	5.1	429	4	US-08-411-295F-195	Sequence 195, App
692	106.5	5.1	612	4	US-08-467-602-228	Sequence 228, App
693	106.5	5.1	612	4	US-08-411-295F-154	Sequence 154, App
694	106.5	5.1	646	4	US-08-467-602-270	Sequence 270, App
695	106.5	5.1	646	4	US-08-411-295F-196	Sequence 196, App
696	106.5	5.1	659	4	US-08-467-602-229	Sequence 229, App
697	106.5	5.1	659	4	US-08-411-295F-155	Sequence 155, App
698	106.5	5.1	693	4	US-08-467-602-271	Sequence 271, App
699	106.5	5.1	693	4	US-08-411-295F-197	Sequence 197, App
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712	106.5	5.1	822	1	US-08-441-944A-4	Sequence 4, Appli
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714	106.5	5.1	822	3	US-08-439-992A-2	Sequence 2, Appli
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716	106.5	5.1	869	4	US-09-715-249-8	Sequence 8, Appli
717	106.5	5.1	1474	4	US-09-677-046A-4	Sequence 4, Appli
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721	105.5	5.0	324	4	US-09-620-461-6	Sequence 2, Appli
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727	105.5	5.0	609	4	US-09-949-016-7749	Sequence 7749, Ap
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729	105.5	5.0	609	4	US-09-949-016-7751	Sequence 7751, Ap
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731	105.5	5.0	609	4	US-09-949-016-7753	Sequence 7753, Ap
732	105.5	5.0	651	4	US-09-949-016-7754	Sequence 7754, Ap
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736	105	5.0	336	4	US-09-949-016-7715	Sequence 7715, Ap
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738	105	5.0	828	1	US-08-261-304-2	Sequence 2, Appli
739	104.5	5.0	1461	4	US-09-976-594-531	Sequence 531, App
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741	104	5.0	386	4	US-08-467-602-218	Sequence 218, App
742	104	5.0	386	4	US-08-411-295F-144	Sequence 144, App
743	104	5.0	420	1	US-07-847-743B-29	Sequence 29, Appl
744	104	5.0	420	1	US-08-456-201-29	Sequence 29, Appl
745	104	5.0	420	2	US-08-456-241-29	Sequence 29, Appl
746	104	5.0	420	4	US-08-467-602-260	Sequence 260, App
747	104	5.0	420	4	US-08-411-295F-186	Sequence 186, App
748	104	5.0	420	5	PCT-US92-04295A-29	Sequence 29, Appl
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750	104	5.0	603	4	US-08-411-295F-142	Sequence 142, App
751	104	5.0	637	1	US-07-847-743B-28	Sequence 28, Appl
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753	104	5.0	637	2	US-08-456-241-28	Sequence 28, Appl
754	104	5.0	637	4	US-08-467-602-258	Sequence 258, App
755	104	5.0	637	4	US-08-411-295F-184	Sequence 184, App
756	104	5.0	637	5	PCT-US92-04295A-28	Sequence 28, Appl
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762	104	5.0	684	4	US-08-467-602-259	Sequence 259, App
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773	104	5.0	1356	4	US-09-949-016-6198	Sequence 6198, Ap
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781	103	4.9	612	4	US-08-467-602-291	Sequence 291, App
782	103	4.9	612	4	US-08-411-295F-217	Sequence 217, App
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784	103	4.9	637	2	US-08-235-838-14	Sequence 14, Appl
785	103	4.9	637	2	US-08-465-473B-14	Sequence 14, Appl
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794	102.5	4.9	640	4	US-09-902-775A-292	Sequence 292, App
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796	102.5	4.9	640	4	US-09-903-603A-292	Sequence 292, App
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799	102.5	4.9	640	4	US-09-905-381A-292	Sequence 292, App
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809	102	4.9	523	4	US-09-910-174B-11	Sequence 11, Appl
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812	102	4.9	664	4	US-09-949-016-7850	Sequence 7850, Ap
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814	102	4.9	702	4	US-09-949-016-6484	Sequence 6484, Ap
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817	102	4.9	740	4	US-09-949-016-8168	Sequence 8168, Ap
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823	101.5	4.8	625	4	US-08-467-602-250	Sequence 250, App
824	101.5	4.8	625	4	US-08-411-295F-176	Sequence 176, App
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826	101.5	4.8	1260	3	US-08-506-296B-21	Sequence 21, Appl
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833	101	4.8	890	3	US-08-170-558-2	Sequence 2, Appli
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836	101	4.8	890	4	US-09-223-490-2	Sequence 1, Appli
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839	101	4.8	911	2	US-08-440-816A-1	Sequence 1, Appli
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843	100.5	4.8	386	4	US-08-411-295F-207	Sequence 207, App
844	100.5	4.8	455	4	US-09-949-016-6949	Sequence 6949, App
845	100.5	4.8	455	4	US-09-949-016-11026	Sequence 11026, A
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847	100.5	4.8	603	4	US-08-411-295F-205	Sequence 205, App
848	100.5	4.8	650	4	US-08-467-602-280	Sequence 280, App
849	100.5	4.8	650	4	US-08-411-295F-206	Sequence 206, App
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852	100	4.8	63	4	US-09-397-243D-10	Sequence 10, Appli
853	100	4.8	124	4	US-09-858-664A-28	Sequence 28, Appli
854	100	4.8	124	4	US-10-274-978-29	Sequence 29, Appli
855	100	4.8	124	4	US-10-697-263-29	Sequence 29, Appli
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862	100	4.8	329	2	US-08-456-104-2	Sequence 2, Appli
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864	100	4.8	329	3	US-08-479-744A-2	Sequence 2, Appli
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866	100	4.8	329	3	US-08-205-697A-23	Sequence 23, Appli
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1018	97	4.5	1091	94	422	5	PCT-US95-06846A-170	Sequence 170, App
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1123	92.5	4.4	282	4	US-09-667-857-393	Sequence 393, App	1196	91.5	4.4	576	5	PCT-US96-08899-4	Sequence 4, Appli
1124	92.5	4.4	309	4	US-09-404-879A-392	Sequence 392, App	1197	91.5	4.4	643	5	PCT-US93-00031-19	Sequence 19, Appl
1125	92.5	4.4	309	4	US-09-667-857-392	Sequence 392, App	1198	91.5	4.4	644	5	PCT-US93-00031-21	Sequence 21, Appl
1126	92.5	4.4	329	4	US-09-651-200-18	Sequence 18, Appl	1199	91.5	4.4	647	3	US-09-009-490A-91	Sequence 91, Appl
1127	92.5	4.4	329	4	US-09-303-040-6	Sequence 6, Appli	1200	91.5	4.4	647	3	US-08-482-073-5	Sequence 5, Appli
1128	92.5	4.4	424	6	5169835-6	Patent No. 5169835	1201	91.5	4.4	647	5	PCT-US93-00031-11	Sequence 11, Appl
1129	92.5	4.4	424	6	5169835-6	Patent No. 5169835	1202	91.5	4.4	647	5	PCT-US93-00031-23	Sequence 23, Appl
1130	92.5	4.4	426	1	US-08-336-583-2	Sequence 2, Appli	1203	91.5	4.4	740	5	PCT-US93-00031-17	Sequence 17, Appl
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1133	92.5	4.4	746	3	US-08-434-000A-4	Sequence 4, Appli	1206	91.5	4.4	1911	2	US-08-800-825A-5	Sequence 5, Appli
1134	92.5	4.4	746	3	US-09-312-157-4	Sequence 4, Appli	1207	91.5	4.4	1911	3	US-09-158-657-5	Sequence 5, Appli
1135	92.5	4.4	746	4	US-09-717-888-4	Sequence 4, Appli	1208	91.5	4.4	1911	5	PCT-US94-10166-5	Sequence 5, Appli
1136	92.5	4.4	764	4	US-09-949-016-6254	Sequence 6254, Ap	1209	91	4.3	218	4	US-09-451-291-12	Sequence 12, Appl
1137	92.5	4.4	816	4	US-09-949-016-8119	Sequence 8119, Ap	1210	91	4.3	371	4	US-08-411-295F-308	Sequence 308, App
1138	92.5	4.4	887	4	US-09-540-236-2911	Sequence 2911, Ap	1211	91	4.3	405	4	US-08-467-602-384	Sequence 384, App
1139	92	4.4	95	3	US-08-928-383B-17	Sequence 17, Appl	1212	91	4.3	405	4	US-08-411-295F-307	Sequence 307, App
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1141	92	4.4	274	4	US-09-549-067A-30	Sequence 30, Appl	1214	91	4.3	477	2	US-08-684-594-3	Sequence 3, Appli
1142	92	4.4	302	1	US-08-121-054C-18	Sequence 18, Appl	1215	91	4.3	771	3	US-08-434-000A-8	Sequence 8, Appli
1143	92	4.4	302	1	US-08-121-054C-30	Sequence 30, Appl	1216	91	4.3	771	3	US-09-312-157-8	Sequence 8, Appli
1144	92	4.4	302	3	US-08-539-436-18	Sequence 18, Appl	1217	91	4.3	771	4	US-09-717-888-8	Sequence 8, Appli
1145	92	4.4	302	3	US-08-539-436-30	Sequence 30, Appl	1218	91	4.3	816	4	US-07-640-029-1	Sequence 1, Appli
1146	92	4.4	302	4	US-09-813-659-18	Sequence 18, Appl	1219	90.5	4.3	76	4	US-09-397-243D-11	Sequence 11, Appl
1147	92	4.4	302	4	US-09-813-659-32	Sequence 32, Appl	1220	90.5	4.3	238	4	US-09-798-689-21	Sequence 21, Appl
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1151	92	4.4	351	4	US-09-949-016-9628	Sequence 9628, Ap	1224	90.5	4.3	310	3	US-08-485-372A-6	Sequence 6, Appli
1152	92	4.4	357	4	US-09-949-016-9074	Sequence 9074, Ap	1225	90.5	4.3	310	3	US-09-409-006A-6	Sequence 6, Appli
1153	92	4.4	411	3	US-08-470-339-189	Sequence 189, App	1226	90.5	4.3	310	4	US-08-484-681-6	Sequence 6, Appli
1154	92	4.4	414	3	US-08-470-339-188	Sequence 188, App	1227	90.5	4.3	310	4	US-09-766-995-6	Sequence 6, Appli
1155	92	4.4	422	4	US-08-467-602-324	Sequence 324, App	1228	90.5	4.3	310	5	PCT-US93-07422-6	Sequence 6, Appli
1156	92	4.4	422	4	US-08-411-295F-250	Sequence 250, App	1229	90.5	4.3	330	2	US-08-525-864A-4	Sequence 4, Appli
1157	92	4.4	425	3	US-08-470-335-226	Sequence 226, App	1230	90.5	4.3	433	3	US-09-100-409A-1	Sequence 1, Appli
1158	92	4.4	425	4	US-08-467-602-320	Sequence 320, App	1231	90.5	4.3	593	4	US-09-269-939A-2	Sequence 2, Appli
1159	92	4.4	425	4	US-08-411-295F-246	Sequence 246, App	1232	90.5	4.3	754	2	US-08-525-864A-2	Sequence 2, Appli
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1163	92	4.4	456	4	US-08-411-295F-229	Sequence 229, App	1236	90	4.3	259	4	US-09-419-788-29	Sequence 29, Appl
1164	92	4.4	456	4	US-08-411-295F-292	Sequence 292, App	1237	90	4.3	288	4	US-09-651-200-14	Sequence 14, Appl
1165	92	4.4	459	3	US-08-470-335-239	Sequence 239, App	1238	90	4.3	290	4	US-09-910-174B-32	Sequence 32, Appl
1166	92	4.4	459	4	US-08-467-602-299	Sequence 299, App	1239	90	4.3	290	4	US-09-451-291-3	Sequence 3, Appli
1167	92	4.4	459	4	US-08-467-602-362	Sequence 362, App	1240	90	4.3	433	2	US-09-645-069-23	Sequence 23, Appl
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1169	92	4.4	459	4	US-08-411-295F-288	Sequence 288, App	1242	90	4.3	434	3	US-08-808-374-1	Sequence 1, Appli
1170	92	4.4	479	4	US-08-467-602-307	Sequence 307, App	1243	90	4.3	471	4	US-09-540-245A-19	Sequence 19, Appl
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1172	92	4.4	490	4	US-08-467-602-345	Sequence 345, App	1245	90	4.3	471	4	US-09-949-016-9043	Sequence 9043, Ap
1173	92	4.4	490	4	US-08-411-295F-271	Sequence 271, App	1246	90	4.3	471	4	US-09-949-016-9044	Sequence 9044, Ap
1174	92	4.4	493	4	US-08-467-602-341	Sequence 341, App	1247	90	4.3	471	4	US-09-949-016-9045	Sequence 9045, Ap
1175	92	4.4	493	4	US-08-411-295F-267	Sequence 267, App	1248	90	4.3	471	4	US-09-949-016-9046	Sequence 9046, Ap
1176	92	4.4	513	4	US-08-467-602-349	Sequence 349, App	1249	90	4.3	471	4	US-09-949-016-9047	Sequence 9047, Ap
1177	92	4.4	513	4	US-08-411-295F-275	Sequence 275, App	1250	90	4.3	471	4	US-09-949-016-9048	Sequence 9048, Ap
1178	92	4.4	526	1	US-08-471-570-4	Sequence 4, Appli	1251	90	4.3	471	4	US-09-949-016-9049	Sequence 9049, Ap
1179	92	4.4	613	4	US-09-800-729-82	Sequence 82, Appl	1252	90	4.3	471	4	US-09-949-016-9050	Sequence 9050, Ap
1180	92	4.4	613	4	US-09-800-729-98	Sequence 98, Appl	1253	90	4.3	471	4	US-09-949-016-9051	Sequence 9051, Ap
1181	92	4.4	652	1	US-08-471-570-10	Sequence 10, Appl	1254	90	4.3	553	2	US-08-661-052-16	Sequence 16, Appl
1182	92	4.4	2491	4	US-09-207-363-1	Sequence 1, Appli	1255	90	4.3	553	3	US-09-188-082-16	Sequence 16, Appl
1183	91.5	4.4	272	4	US-09-726-219A-183	Sequence 183, App	1256	90	4.3	553	3	US-09-364-088-16	Sequence 16, Appl
1184	91.5	4.4	287	4	US-09-318-786-37	Sequence 37, Appl	1257	90	4.3	553	3	US-09-102-716-16	Sequence 16, Appl
1185	91.5	4.4	338	1	US-08-442-043A-17	Sequence 17, Appl	1258	90	4.3	582	4	US-09-702-705-334	Sequence 334, App
1186	91.5	4.4	338	1	US-08-441-893A-17	Sequence 17, Appl	1259	90	4.3	582	4	US-09-671-325-334	Sequence 334, App
1187	91.5	4.4	388	3	US-09-188-930A-17	Sequence 17, Appl	1260	90	4.3	582	4	US-09-589-184-334	Sequence 334, App
1188	91.5	4.4	388	4	US-09-188-930A-275	Sequence 275, App	1261	90	4.3	582	4	US-09-658-824-334	Sequence 334, App
1189	91.5	4.4	576	1	US-09-312-283C-275	Sequence 275, App	1262	90	4.3	582	4	US-09-589-824-334	Sequence 334, App
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1191	91.5	4.4	576	3	US-08-924-376-4	Sequence 4, Appli	1264	90	4.3	821	2	US-08-323-430-13	Sequence 13, Appl
1192	91.5	4.4	576	3	US-08-685-212-4	Sequence 4, Appli	1265	90	4.3	821	3	US-08-323-430-13	Sequence 13, Appl
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1273	89.5	4.3	597	4	US-09-746-311B-381	Sequence 381, App
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1277	89	4.2	287	4	US-09-800-729-153	Sequence 153, App
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1279	89	4.2	342	4	US-09-684-708A-27	Sequence 27, Appl
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1281	89	4.2	466	2	US-08-684-594-4	Sequence 4, Appli
1282	89	4.2	583	2	US-08-432-016-2	Sequence 2, Appli
1283	89	4.2	583	2	US-08-684-594-2	Sequence 2, Appli
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1286	89	4.2	615	3	US-08-985-950-16	Sequence 16, Appl
1287	89	4.2	615	3	US-08-985-950-18	Sequence 18, Appl
1288	89	4.2	615	4	US-09-546-049-16	Sequence 16, Appl
1289	89	4.2	615	4	US-09-546-049-18	Sequence 18, Appl
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1298	88.5	4.2	403	4	US-09-638-648-5	Sequence 5, Appli
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1303	88	4.2	181	3	US-09-398-496-4	Sequence 4, Appli
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1310	88	4.2	407	3	US-09-398-496-6	Sequence 6, Appli
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1315	88	4.2	605	3	US-09-707-802-8	Sequence 8, Appli
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1320	88	4.2	769	3	US-09-312-157-10	Sequence 10, Appl
1321	88	4.2	769	4	US-09-717-888-10	Sequence 10, Appl
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1323	88	4.2	787	1	US-08-268-161A-110	Sequence 110, App
1324	88	4.2	787	2	US-08-453-702A-110	Sequence 110, App
1325	88	4.2	787	3	US-09-099-639-110	Sequence 110, App
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1331	87.5	4.2	205	3	US-09-016-649-2	Sequence 2, Appli
1332	87.5	4.2	205	5	PCT-US95-04858-2	Sequence 2, Appli
1333	87.5	4.2	223	4	US-09-248-796A-23094	Sequence 23094, A
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1337	87	4.1	382	4	US-08-467-602-382	Sequence 382, App
1338	87	4.1	535	3	US-08-983-035A-38	Sequence 38, Appl
1339	87	4.1	653	4	US-09-520-781-10	Sequence 10, Appl
1340	87	4.1	666	3	US-09-423-439-51	Sequence 51, Appl
1341	87	4.1	668	3	US-09-173-151A-35	Sequence 35, Appl

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1345	86.5	4.1	230	4	US-10-071-485-102	Sequence 102, App
1346	86.5	4.1	669	4	US-09-071-035-264	Sequence 264, App
1347	86.5	4.1	826	4	US-09-877-730-16	Sequence 16, Appl
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1352	86.5	4.1	894	3	US-08-170-558-34	Sequence 34, Appl
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1354	86.5	4.1	894	3	US-08-445-461-34	Sequence 34, Appl
1355	86.5	4.1	894	4	US-09-223-490-34	Sequence 34, Appl
1356	86.5	4.1	904	4	US-09-877-730-6	Sequence 6, Appli
1357	86.5	4.1	907	4	US-09-877-730-20	Sequence 20, Appl
1358	86.5	4.1	975	4	US-09-949-016-7595	Sequence 7595, Ap
1359	86.5	4.1	985	4	US-09-877-730-10	Sequence 10, Appl
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1362	86.5	4.1	1069	4	US-09-877-730-2	Sequence 2, Appli
1363	86.5	4.1	1072	4	US-09-877-730-18	Sequence 18, Appl
1364	86.5	4.1	1150	4	US-09-877-730-8	Sequence 8, Appli
1365	86.5	4.1	1363	4	US-09-375-248-19	Sequence 19, Appl
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1368	86	4.1	241	3	US-08-470-339-195	Sequence 195, App
1369	86	4.1	241	4	US-08-467-602-389	Sequence 389, App
1370	86	4.1	241	4	US-08-411-295F-47	Sequence 47, Appl
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1372	86	4.1	270	2	US-08-652-507-2	Sequence 2, Appli
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1374	86	4.1	398	1	US-08-442-043A-2	Sequence 2, Appli
1375	86	4.1	398	3	US-09-173-151A-26	Sequence 26, Appl
1376	86	4.1	398	4	US-09-461-908-2	Sequence 2, Appli
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1378	86	4.1	398	4	US-08-406-824A-8	Sequence 8, Appli
1379	86	4.1	398	4	US-09-921-667-8	Sequence 8, Appli
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1381	86	4.1	418	3	US-09-949-016-9458	Sequence 9458, Ap
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1383	86	4.1	483	4	US-08-842-248A-16	Sequence 16, Appl
1384	86	4.1	590	4	US-09-520-781-12	Sequence 12, Appl
1385	86	4.1	630	4	US-09-499-522-16	Sequence 16, Appl
1386	86	4.1	630	4	US-09-269-939A-10	Sequence 10, Appl
1387	86	4.1	1434	4	US-10-080-505-9	Sequence 9, Appli
1388	85.5	4.1	225	4	US-09-530-139-42	Sequence 42, Appl
1389	85.5	4.1	300	1	US-07-640-029-5	Sequence 5, Appli
1390	85.5	4.1	300	3	US-08-439-992A-5	Sequence 5, Appli
1391	85.5	4.1	302	1	US-07-640-029-6	Sequence 6, Appli
1392	85.5	4.1	302	1	US-07-921-807B-7	Sequence 7, Appli
1393	85.5	4.1	302	1	US-07-921-807B-8	Sequence 8, Appli
1394	85.5	4.1	302	1	US-08-441-944A-7	Sequence 7, Appli
1395	85.5	4.1	302	1	US-08-441-944A-8	Sequence 8, Appli
1396	85.5	4.1	302	3	US-08-439-992A-6	Sequence 6, Appli
1397	85.5	4.1	312	3	US-09-079-029-10	Sequence 10, Appl
1398	85.5	4.1	335	4	US-09-252-991A-27567	Sequence 27567, A
1399	85.5	4.1	449	2	US-08-482-090-11	Sequence 11, Appl
1400	85.5	4.1	450	1	US-08-105-710-7	Sequence 7, Appli
1401	85.5	4.1	450	1	US-08-365-901-7	Sequence 7, Appli
1402	85.5	4.1	450	2	US-09-007-383-15	Sequence 15, Appl
1403	85.5	4.1	450	3	US-08-479-703A-6	Sequence 6, Appli
1404	85.5	4.1	477	4	US-09-949-016-9192	Sequence 9192, Ap
1405	85.5	4.1	477	4	US-09-949-016-9193	Sequence 9193, Ap
1406	85.5	4.1	477	4	US-09-949-016-9194	Sequence 9194, Ap
1407	85.5	4.1	477	4	US-09-949-016-9195	Sequence 9195, Ap
1408	85.5	4.1	477	4	US-09-949-016-9196	Sequence 9196, Ap
1409	85.5	4.1	477	4	US-09-949-016-9197	Sequence 9197, Ap
1410	85.5	4.1	477	4	US-09-949-016-9198	Sequence 9198, Ap
1411	85.5	4.1	477	4	US-09-949-016-9199	Sequence 9199, Ap
1412	85.5	4.1	615	4	US-08-840-713-35	Sequence 35, Appl
1413	85.5	4.1	617	4	US-08-840-713-37	Sequence 37, Appl
1414	85.5	4.1	932	4	US-09-071-035-416	Sequence 416, App

Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILLISLCMVVET 300
QY 301 MAYIMLCRKTSQOEHVYEAAR 321
Db 301 MAYIMLCRKTSQOEHVYEAAR 321

RESULT 2
US-09-953-499-2
; Sequence 2, Application US/09953499
; Patent No. 6838554
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/953,499
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/254,465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-2

Query Match 80.5%; Score 1688; DB 4; length 321;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGILLGLLLGLHLYVDYGRPILEVPESVTGPKGDVNLPCITYDPLQGYTQVLVKMLVOR 60
Db 1 MGILLGLLLGLHLYVDYGRPILEVPESVTGPKGDVNLPCITYDPLQGYTQVLVKMLVOR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLLQSTLEMDDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLLQSTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFVPGMRISLQCCQARGSPPISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFVPGMRISLQCCQARGSPPISYIWKQ 180
QY 181 QTNNOEPKIVATLSTLFEKPAVIADSGSYFCTAKGVGSEQHSIDIVKFWVKDSSKLLKTK 240
Db 181 QTNNOEPKIVATLSTLFEKPAVIADSGSYFCTAKGVGSEQHSIDIVKFWVKDSSKLLKTK 240
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILLISLCMVVET 300
Db 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILLISLCMVVET 300
QY 301 MAYIMLCRKTSQOEHVYEAAR 321
Db 301 MAYIMLCRKTSQOEHVYEAAR 321

RESULT 3
US-09-369-247-63

; Sequence 63, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (306)
; OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-63

Query Match 73.7%; Score 1547; DB 4; length 306;
Best Local Similarity 76.2%; Pred. No. 1.2e-152;
Matches 304; Conservative 0; Mismatches 1; Indels 94; Gaps 1;
QY 1 MGILLGLLLGLHLYVDYGRPILEVPESVTGPKGDVNLPCITYDPLQGYTQVLVKMLVOR 60
Db 1 MGILLGLLLGLHLYVDYGRPILEVPESVTGPKGDVNLPCITYDPLQGYTQVLVKMLVOR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLLQSTLEMDDRSHYTCEVTWQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPDVSLLQSTLEMDDRSHYTCEVTWQTP 120
QY 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFVPGMRISLQCCQARGSPPISYIWKQ 180
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFVPGMRISLQCCQARGSPPISYIWKQ 180
QY 181 QTNNOEPKIVATLSTLFEKPAVIADSGSYFCTAKGVGSEQHSIDIVKFWVKDSSKLLKTK 240
Db 137 -----KHSSKLLKTK 146
QY 241 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILLISLCMVVET 300
Db 147 TEAPTTMTYPLKATSTVKQSWDWTMDGYLGETSAGPGKSLPVFAIILLISLCMVVET 306
QY 301 MAYIMLCRKTSQOEHVYEAARAHAREANDSGETMRVAIFASGCCSDEPTSQNLGNYSDE 360
Db 207 MAYIMLCRKTSQOEHVYEAARAHAREANDSGETMRVAIFASGCCSDEPTSQNLGNYSDE 266
QY 361 PCIGQEQYQIIAQINGNYARLLDTPLDYEFLEATEGKSVC 399
Db 267 PCIGQEQYQIIAQINGNYARLLDTPLDYEFLEATEGKSVC 305

RESULT 4
US-09-763-902B-6
; Sequence 6, Application US/09763902B
; Patent No. 6838241
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: YUE, Henry

```

; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: GORGONE, Gina A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: PROTEIN TRANSPORT-ASSOCIATED MOLECULES
; FILE REFERENCE: PF-0577 PCT
; CURRENT APPLICATION NUMBER: US/09/763,902B
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/098,206
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 68382411871275CD1
US-09-763-902B-6

Query Match          41.5%; Score 870; DB 4; length 175;
Best Local Similarity 64.7%; Pred. No. 2,1e-82;
Matches 174; Conservative 0; Mismatches 1; Indels 94; Gaps 1;
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QY 1 MGILLGLLLGLHLYTDYGRPILEVEPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 1 MGILLGLLLGLHLYTDYGRPILEVEPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPBGDVSILQSTLEMDDRSHYTCETWTQTP 120
Db 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHKVPBGDVSILQSTLEMDDRSHYTCETWTQTP 120
QY 121 DGNQVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRLISLQCCARGSPISYIWKQ 180
Db 121 DGNQVRDKITELRVQ----- 136
QY 181 QTNNOEPIKAVATLSTLFRPAVIADSGSYFCTAKQVSEQHSIDIVKVVKDSKLLKTK 240
Db 137 -----KHSSKLLKTK 146
QY 241 TEAPTMITYPLKATSTVKQSWDWTMDG 269
Db 147 TEAPTMITYPLKATSTVKQSWDWTMDG 175
```

```

RESULT 5
US-09-188-930-189
; Sequence 189, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000,1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; NAME/KEY: UNSURE
; LOCATION: (289)...(289)
```

```

US-09-188-930-189

Query Match          8.5%; Score 178.5; DB 3; length 299;
Best Local Similarity 26.5%; Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGLHLYTDYGRPILEVEPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 17 LAIILCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSLAY---SGFSSPRVEN----- 62
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHK-----VPGDVSILQSTLEMDDRSHYTCETV 115
Db 63 -----KPDQGDITRLVLCYNKNKITASIEDRVTFELPTGITPKSVTRE--DTGITTCMV 111
QY 116 TWQTPDGNQVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRLISLQCCAR-GSPPIIS 174
Db 112 SEEGNSYGEVVKVLIIVL---VPPSKPTVNIPS-----SATIGNRAVLTCSEODGSPPE 163
QY 175 YIWKY----QQTN-----NOEPIKAVATLSTLFRPAVIADSGSYFCTAKQVSEQH 222
Db 164 YTWFKDGIIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPTMT 223
QY 223 SDIVK 227
Db 224 SNAVR 228
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```

RESULT 6
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000,1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-331

Query Match          8.5%; Score 178.5; DB 3; length 299;
Best Local Similarity 26.5%; Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGLHLYTDYGRPILEVEPESVTGPMKGDVNLPCITYDPLQGYTQVLVKMLVQR 60
Db 17 LAIILCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSLAY---SGFSSPRVEN----- 62
QY 61 GSDPVTIFLRDSSGDHIQQAQYQGRHLVSHK-----VPGDVSILQSTLEMDDRSHYTCETV 115
Db 63 -----KPDQGDITRLVLCYNKNKITASIEDRVTFELPTGITPKSVTRE--DTGITTCMV 111
QY 116 TWQTPDGNQVRDKITELRVQKLSVSKPTVTGSGYGFVPOGMRLISLQCCAR-GSPPIIS 174
Db 112 SEEGNSYGEVVKVLIIVL---VPPSKPTVNIPS-----SATIGNRAVLTCSEODGSPPE 163
QY 175 YIWKY----QQTN-----NOEPIKAVATLSTLFRPAVIADSGSYFCTAKQVSEQH 222
Db 164 YTWFKDGIIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPTMT 223
QY 223 SDIVK 227
Db 224 SNAVR 228
```



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RESULT 7
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
; TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2

```

```

Query Match          8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY      1 MGILLGLLLGLHVTVDYGRPILEVPESEVTGPMKGDVNLPCITYDPLQGYTQVLVKWLVQR 60
      : ||| : || : || : || : || : || : || : || : || : || : || : || : ||
DB      17 LAILCSLALGSVTVHS-SEPEVRI PEN-----NPVKLSGAY---SGFSSPRVEW----- 62

QY      61 GSDPVTIFLRDSSGDHIQAKYQGRHLVSHK-----VPGDVSLQLSTLEMDRSHYTCBV 115
      : : || : || : || : || : || : || : || : || : || : || : || : ||
DB      63 -----KPDQGDTRFLVCYNKKITASYEDRVTFLLPTGIFKSVTRE--DTGTYTCMV 111

QY      116 TWQTPDGNQVVRDKITELRVQKLSKPTVTTGSGYGFVPGCMRISLQCCAR-GSPPI 174
      : : : : || : || : || : || : || : || : || : || : || : || : ||
DB      112 SEEGNSYGEVKKLIVL-----VPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

QY      175 YIWK-----QQTN-----NOEPIKATLSTLLFKPAVIDSGSYCTAKGVGSEQH 222
      : || : || : || : || : || : || : || : || : || : || : || : ||
DB      164 YTWFKDGI VMP TNP KSTRAFNSSYLVNPTTGLVFDFPLASDTGEYSCEARNGYGTPT 223

QY      223 SDIVK 227
      : : || :
DB      224 SNAVR 228

RESULT 8
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254, 465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078, 936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437

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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-1

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Query Match	8.5%;	Score 178.5;	DB 4;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 7e-10;		
Matches 65;	Conservative 36;	Mismatches 93;	Indels 51;	Gaps 11;

```

QY      1 MGILLG L L L L G H L T V D T Y G R P I L E V P E S V T G P M K G D V N L P C T Y D P L O G Y T O V L V K M L V O R      60
      : | | | : | | : | | : | | : | | : | | : | | : | |
Db      17 L A I L C S L A L G S V T V H S - S E P E V R I P E N ----- N P V K L S C A Y - - S G F S S P R V E W -----      62

QY      61 G S D P V T I F L R D S S G D H I O Q A K Y O G R L H V S H K ----- V P G D V S L O L S T L E M D R S H Y T C E V      115
      : | | : | | : | | : | | : | | : | | : | | : | |
Db      63 ----- K P D Q G D T T R I V C Y N N K I T A S Y E D R V T F L P T G I T F K S V T R E - - D T G T Y T C M V      111

QY      116 T W Q T P D G N Q V R D K I T E L R V O K L S V S K P T V T T G S G Y G F T V P Q G M R I S L O C Q A R - G S P P I S      174
      : : : : | : | : | : | | | | | : | | | | | : | | | |
Db      112 S E E G N S Y G E V K V K L I V L ----- V P P S K P T V N I P S ----- S A T I G N R A V L T C S E Q D G S P P S E      163

QY      175 Y I W Y K - - - Q Q T N - - - - - N Q E P I K A V T L S T L L F K P A V I A D S G S Y F C T A K Q V G S E Q H      222
      : | : | : | | : | | : | | : | | : | | : | | : | |
Db      164 Y T W F K D G I V M P T N P K S T R A P S N S S Y V L N P T T G E L V F D P L S A D T G E Y S C E A R N G Y G T P M T      223

QY      223 S D I V K      227
      : : | :
Db      224 S N A V R      228

```

```

RESULT 9
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-189

```

Query Match	8.5%;	Score 178.5;	DB 4;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 7e-10;		
Matches 65;	Conservative 36;	Mismatches 93;	Indels 51;	Gaps 11;

QY	1	MGILLGLLLGHLTVDTYGRPILEVPESVETGPMWGDVNLPCYTDPLQGYTVLVKMLVQR	60
		: : : : : : :	
Db	17	LAILLCSIALGSVTVHS-SEPEVRIPEN-----NPVKLSGAY--SGFSSPRVEW----	62
QY	61	GSDPVTIFLRDSSGDHIQQAQYGRLHVSHK-----VPGDVSLQSLTEMDRSHYTCFV	115
		: : : : : : :	
Db	63	-----KFDGDTIRLVCCYNKKITASYEDRVTFLLPTGTFKSVIRE--DTGYTCMV	111
QY	116	TWQTPDGNQVRDKITELRVOKLSVSKPTVTGSGYGFVTPQCMRISLQCOAR-GSPPI	174
		: : : : : : : : :	
Db	112	SEEGNSYGEVKVILV---VPPSKPTVNIPS---SATIGNRAVLTCSEQDGSPPSE	163

QY 175 YIWK-----QQTN-----NQEPKATLSTLLFKPAVIADSGSYECTAKGVGSEQH 222
DB 164 YTFMKDGIVMPTNPKSTRAPSNSSYVLNPTTGLVFDPLASADTGEYSCEARNGYGTPEMT 223
QY 223 SDIVK 227
DB 224 SNAVR 228

RESULT 10
US-09-312-283C-331

```

: Sequence 331, Application US/09312283C
: Patent No. 6573095
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Murison, James G.
: APPLICANT: Kumble, Krishanand D.
: TITLE OF INVENTION: Compositions Isolated from Skin Cells
: TITLE OF INVENTION: and Methods for Their Use
: FILE REFERENCE: 11000.1011c2
: CURRENT APPLICATION NUMBER: US/09/312,283C
: CURRENT FILING DATE: 1999-05-14
: NUMBER OF SEQ ID NOS: 425
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 331
: LENGTH: 299
: TYPE: PRT
: ORGANISM: Mouse
US-09-312-283C-331

```

Query Match	8.5%;	Score 178.5;	DB 4;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 7e-10;		
Matches 65;	Conservative 36;	Mismatches 93;	Indels 51;	Gaps 11;

```

QY      1 MGIILGILLGLHLTVDTYGRPILEVPESVTGPMKGDVNLPTCTYDPLQGYTOVLKRLVQR 60
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPKLSCAY--SGFSSPRVEW----- 62

QY      61 GSDPVTIFLRDSSGDHIOQAKYQGRHLVHSHK-----VPGDVSLQLSTLEMDRSHYTCEV 115
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      63 -----KFDQGDTRTLVCYNNKKTASVEDRVTLPTGITFKSVTRE--DTGTYTCMV 111

QY      116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTYTGSGYGFVTPQGMRLSLQCCAR--CSBPIS 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      112 SEEGNSYGEVKVKLIVL---VPSPKPTVNIPS-----SATIGNRAVLTCSEQDGSPPSE 163

QY      175 YIWKY----QOTN-----NQEPKVAATLSTLLFKPAVIADSGSYFCTAKGQVSEQH 222
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      164 YTWFKDGI VMPPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPTMT 223

QY      223 SDIVK 227
      : : : : :
Db      224 SNAVR 228

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RESULT 11
US-09-907-794A-119
; Sequence 119, Application US/09907794A

; APPLICANT: Genentech, Inc.
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Flivaroff, Ellen
 ; APPLICANT: Pong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter

```

1  APPLICANT: Gerritsen, Mary E.
2  APPLICANT: Goddard, A.
3  APPLICANT: Godowski, Paul J.
4  APPLICANT: Grimaldi, Christopher J.
5  APPLICANT: Gurney, Austin L.
6  APPLICANT: Hillan, Kenneth, J.
7  APPLICANT: Kljavin, Ivar J.
8  APPLICANT: Mathew, Jennie P.
9  APPLICANT: Pan, James
10 APPLICANT: Paonl, Nicholas F.
11 APPLICANT: Roy, Margaret Ann
12 APPLICANT: Stewart, Timothy A.
13 APPLICANT: Tumas, Daniel
14 APPLICANT: Williams, P. Mickey
15 APPLICANT: Wood, William, I.
16 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
17 FILE REFERENCE: 10466-14
18 CURRENT APPLICATION NUMBER: US/09/907, 794A
19 PRIOR FILING DATE: 2001-07-17
20 PRIOR APPLICATION NUMBER: PCT/US00/04414
21 PRIOR FILING DATE: 2000-02-22
22 PRIOR APPLICATION NUMBER: US 60/143, 048
23 PRIOR FILING DATE: 1999-07-07
24 PRIOR APPLICATION NUMBER: US 60/145, 698
25 PRIOR FILING DATE: 1999-07-26
26 PRIOR APPLICATION NUMBER: US 60/146, 222
27 PRIOR FILING DATE: 1999-07-28
28 PRIOR APPLICATION NUMBER: PCT/US99/20594
29 PRIOR FILING DATE: 1999-09-08
30 PRIOR APPLICATION NUMBER: PCT/US99/20944
31 PRIOR FILING DATE: 1999-09-13
32 PRIOR APPLICATION NUMBER: PCT/US99/21090
33 PRIOR FILING DATE: 1999-09-15
34 PRIOR APPLICATION NUMBER: PCT/US99/21547
35 PRIOR FILING DATE: 1999-09-15
36 PRIOR APPLICATION NUMBER: PCT/US99/23089
37 PRIOR FILING DATE: 1999-10-05
38 PRIOR APPLICATION NUMBER: PCT/US99/28214
39 PRIOR FILING DATE: 1999-11-29
40 PRIOR APPLICATION NUMBER: PCT/US99/28313
41 PRIOR FILING DATE: 1999-11-30
42 PRIOR APPLICATION NUMBER: PCT/US99/28564
43 PRIOR FILING DATE: 1999-12-02
44 PRIOR APPLICATION NUMBER: PCT/US99/28565
45 PRIOR FILING DATE: 1999-12-02
46 PRIOR APPLICATION NUMBER: PCT/US99/30095
47 PRIOR FILING DATE: 1999-12-16
48 PRIOR APPLICATION NUMBER: PCT/US99/30911
49 PRIOR FILING DATE: 1999-12-20
50 PRIOR APPLICATION NUMBER: PCT/US99/30999
51 PRIOR FILING DATE: 1999-12-20
52 PRIOR APPLICATION NUMBER: PCT/US00/00219
53 PRIOR FILING DATE: 2000-01-05
54 NUMBER OF SEQ ID NOS: 423
55 SEQ ID NO 119
56 LENGTH: 299
57 TYPE: PRT
58 ORGANISM: Homo sapiens
59 US-09-907-794A-119
60
61 Query Match      8.5%; Score 178.5; DB 4; Length 299;
62 Best Local Similarity 26.5%; Pred. No. 7e-10;
63 Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;
64
65 1 MGILLGLLLGHLTYDYGRIPLVPEVSATGPMKGDVNLPTTYDPLQGYTQVLVKNLQVR 60
66 : ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |
67 17 LAILLCSLALGSVTYHS-SEPEVRIPEN-----NPVKLSLAY---SGFSSPRVEM----- 62
68
69 61 GSDPVTIFLRDSSGDHIIQQAQYQGRHLVSHK-----VPGDVSLLQLSTLEMDSHYTCV 115
70 : ||| | | | : | : | : | : | : | : | : | : | : | : | : | : |
71 63 -----KPDGDTTRILVVCYNMKITASYEDEKRYTFLPTGITTFKSVTRE--DTGTYTCMV 111

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```

; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-907-794A-119

```

Query Match	8.5%;	Score 178.5;	DB 4;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 7e-10;		
Matches	65;	Conservative	36;	Mismatches 93;
			Indels	51;
			Gaps	11;

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QY      1 MGILLGLLLGLHLTVDTYGRPILEVESVTGPMWKGDVNLPTCTYDPLQGYTQVLVKMLVQR 60
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      17 LALLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSICAY--SGFSSPRVEV----- 62
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY      61 GSDPVTIFLRDSSGDHIQQAQAKYQGRHLVSHK-----VPGDVSLQLSTLEMDRSHYTCEV 115
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      63 -----KPDQGGTTRLVLCYNNKKTASIEDRVTFPLPTGITFKSVITRE--DTGYTTCMV 111

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QY      116 TWOTPDGNQVVRDKITELRVQKLSVSKPVTYTTGSGYGFTVPQGMRI SLOQAR-GSPPI S 174
        : : | : | : ||| : | | | : |||
Db      112 SEEGNSYGEVKKVLIVL---VPPSKPTVINIPS-----SATIGNRAVLTCSEQDGSPPSE 163
QY      175 YIWK-----QQTN-----NOEPIKVALTLSTLLFKPAVIADSGSYFCTAKGQVSSEQH 222
        ||:| || | : | :|| :|| :|| :|| :
Db      164 YTWFKDGIWMPTPNPKSTRAFSNSSYVLNPPTIGELVFDPPLSASDTGEYSCEARNGYGRPM T 223
QY      223 SDIVK 227
        |:|:
Db      224 SNAVR 228
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RESULT 12
US-09-905-125A-119
; Sequence 119, Application US/09905125A

```

: Patent No. 6664376
:
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gekriksen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Guiney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pab, James
: APPLICANT: Pabni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905,125A
: PRIOR FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565

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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
;
; LENGTH: 299
;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-119

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Query Match	8.5%;	Score 178.5;	DB 4;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 7e-10;		
Matches 65;	Conservative 36;	Mismatches 93;	Indels 51;	Gaps 11;

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QY      1 MGILLGTLGLHGLTYDVTYGRPILEVPESVTGPMKGDVNLPTCTYDPLQGYIQLVKMLVQR 600
      : ||| ||| : || : ||| ||| ||| : ||| : |||
Db     17 LAILLCSIALGSVTVHS-SEPEVRIPEN-----NPVKLSICAY---SGFSSPRVEM----- 62

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QY      61 GSDPVTIFLRDSSGDHIQQAKYQGRHLVSHK-----VPGDVSLQSLTEMDRSHYTCEV 115
      : || : | : : | : : | : |||
Db      63 -----KFDQGDTRLVLCYNNKKTASIEDRVTFLLPTGITEFKSVYRE--DTGTYTCMV 111

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QY      116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTVTGSGYGFTVPQGMRIQLQCAR-GSPPI 174
      : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      112 SEEGGNSYGEVKKLIVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEQDGSPPSE 163
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QY      175 YIWK-----QQTN-----NQEPKAVATLSTLLFKPAVIADSGSYCTAKGQVGSEQH 222
         |||      ||          :    |||      |||      |||      |
Db      164 YTWFKDGI VMP TNP KSTR AFSNSSV LNP TT GEL VFDP LASDPTGEISCEARNGYGT PMT 223
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QY	223	SDIVK	227
		: :	
Db	224	SNAVR	228

RESULT 13
US-09-902-775A-119
; Sequence 119, Application US/09902775A
; Patent No. 6686451

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: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
:

```


; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-906-700-119

Query Match 8.5%; Score 178.5; DB 4; length 299;
Best Local Similarity 26.5%; Pred.No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

QY 1 MGILLGLLLGLHGLTVDTYGRPLEVEPESVTGPMKGDVNLPCITYDPLQGYTQVLVKLVQR 60
Db 17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSLAY---SGFSSPRVEW----- 62
QY 61 GSDPVTIFLRSSGDH1QAKYQGRHLAVSHK-----VPGDVS1QLSTLEMDRSHYTCYEV 115
Db 63 -----KFDQGDPTTRLVVCYNNKITASYEDRVTFLEPLTGITFKSVTRE--DTGTYTCMV 111
QY 116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTGSGYGFIVPQGMRIISLQCCAR-GSPPIIS 174
Db 112 SEEGNSYGEVKKLIVL-----VPPSKPTVNIPS-----SATIGNRAVLTCSEQDGSPPSE 163
QY 175 YIWKYK---QQTN-----NQEPIKAVTSLLFKRAVIADSGSYFCTAKGVGSEQH 222
Db 164 YTWFKDGIWMPNPKSTAFNSSSYVLNPTTGELVFDPLSASDTEYSCEARNGYGTGMT 223
QY 223 SDIVK 227
Db 224 SNAVR 228

GenCore version 5.1.6
OM protein - protein search, using SW model
Run on: March 2, 2005, 15:22:02 ; Search time 174 Seconds
(without alignments)
886.882 Million cell updates/sec

Title: US-10-633-008-32

Perfect score: 2098

Sequence: 1 MGILLGLLGLHLYVTYGR.....LLDTVPLDYEFLEATEGKSV 399
BLOSUM62

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description

No. Score Match Length DB ID

RESULT 1

ID AAB19396 standard; protein; 399 AA.

DE Amino acid sequence of a human secreted protein.

PN WO200061755-A2.

PD 19-OCT-2000.

PA (CHIR)-CHIRON CORP.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 3; Length 399;

RESULT 2

ID AAE04230 standard; protein; 399 AA.

DE Human gene 11 encoded secreted protein HMSOW51, SEQ ID NO:85.

PN WO200136432-A2.

PD 25-MAY-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Pred. No. 2.2e-172;

RESULT 3

ID AAE04208 standard; protein; 399 AA.

DE Human gene 11 encoded secreted protein HMSOW51, SEQ ID NO:63.

PN WO200136432-A2.

PD 25-MAY-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 4; Length 399;

RESULT 4

ID ABG64488 standard; protein; 399 AA.

DE Human albumin fusion protein #1163.

PN WO200177137-A1.

PD 18-OCT-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 5; Length 399;

RESULT 5

ID ABG64487 standard; protein; 399 AA.

DE Human albumin fusion protein #1162.

PN WO200177137-A1.

PD 18-OCT-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 5; Length 399;

RESULT 6

ID ABU03567 standard; protein; 399 AA.

DE Angiogenesis-associated human protein sequence #112.

PN WO200279492-A2.

PD 10-OCT-2002.

PA (GEOSB-) EOS BIOTECHNOLOGY INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 6; Length 399;

RESULT 7

ID ADA57183 standard; protein; 399 AA.

DE Human secreted protein #466.

PN WO2002102994-A2.

PD 27-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 6; Length 399;

RESULT 8

ID ADA41052 standard; protein; 399 AA.

DE Human secreted protein.

PN WO2002102993-A2.

PD 27-DEC-2002.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 6; Length 399;

RESULT 9

ID ABR47904 standard; protein; 399 AA.

DE Human secreted protein, SEQ ID 795.

PN WO200295010-A2.

PD 28-NOV-2002.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 6; Length 399;

RESULT 10

ID ABR00157 standard; protein; 399 AA.

DE Human gene 147 encoded secreted protein HSDEK49, SEQ ID NO:446.

PN WO200276488-A1.

PD 03-OCT-2002.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 6; Length 399;

RESULT 11

ID ADB91646 standard; protein; 399 AA.

DE Human secreted protein #SEQ ID 592.

PN WO2003004622-A2.

PD 16-JAN-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 7; Length 399;

RESULT 12

ID ADC74298 standard; protein; 399 AA.

DE Human secreted protein - SEQ ID 931.

PN WO2003038063-A2.

PD 08-MAY-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 7; Length 399;

RESULT 13

ID ADL77755 standard; protein; 399 AA.

DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1237.

PN US2004010134-A1.

PD 15-JAN-2004.

PA (ROSE/) ROSEN C A.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 8; Length 399;

RESULT 14

ID ADL77754 standard; protein; 399 AA.

DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1236.

PN US2004010134-A1.

PD 15-JAN-2004.

PA (ROSE/) ROSEN C A.

Query Match

Best Local Similarity 100.0%; Score 2098; DB 8; Length 399;

RESULT 15

ID ADL67172 standard; protein; 399 AA.
DE Human B7-H6 protein SEQ ID NO:42.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 16
ID ADN35311 standard; protein; 399 AA.
DE Human STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 17
ID ABM82416 standard; protein; 399 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO34043, SEQ:6205.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 18
ID ADP23762 standard; protein; 399 AA.
DE PRO polypeptide SEQ ID NO:940.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 19
ID AAM93874 standard; protein; 399 AA.
DE Human polypeptide, SEQ ID NO: 3986.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 2085; DB 4; Length 399;
Best Local Similarity 99.2%; Pred. No. 2.9e-171;
RESULT 20
ID ADL31953 standard; protein; 399 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3986.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 99.4%; Score 2085; DB 8; Length 399;
Best Local Similarity 99.2%; Pred. No. 2.9e-171;
RESULT 21
ID AAE04290 standard; protein; 386 AA.
DE Human gene 11 encoded secreted protein fragment, SEQ ID NO:154.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 2035; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.8e-167;
RESULT 22
ID AAY23322 standard; protein; 321 AA.
DE Amino acid sequence of the PRO362 polypeptide.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 23
ID AAY41691 standard; protein; 321 AA.
DE Human PRO 362 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 24
ID AAB33429 standard; protein; 321 AA.

DE Human PRO362 protein UNQ317 SEQ ID NO:80.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 25
ID AAB44247 standard; protein; 321 AA.
DE Human PRO362 (UNQ317) protein sequence SEQ ID NO:52.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 26
ID AAY95346 standard; protein; 321 AA.
DE Human PRO362 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 27
ID AAB24047 standard; protein; 321 AA.
DE Human PRO362 protein sequence SEQ ID NO:14.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 28
ID ABO25193 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 29
ID ABU72199 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 30
ID ABU84879 standard; protein; 321 AA.
DE Human secreted and transmembrane polypeptide PRO362.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 31
ID ABU61077 standard; protein; 321 AA.
DE Human PRO362 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 32
ID ABU80346 standard; protein; 321 AA.
DE Human secreted/transmembrane protein PRO362.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 33
ID ABU07737 standard; protein; 321 AA.
DE Human A-33 related antigen PRO362.

PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 34
ID ADA24591 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 35
ID ABO19648 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 36
ID ADA12252 standard; protein; 321 AA.
DE Human secreted/transmembrane polypeptide PRO362.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 37
ID ABO19539 standard; protein; 321 AA.
DE Novel human secreted and transmembrane polypeptide #7.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 38
ID ADB73558 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 39
ID ADB76274 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 40
ID ADC43700 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 41
ID ADC61460 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 42
ID ADC63424 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054405-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 43
ID ADC66524 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 44
ID ADC68648 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 45
ID ADC62708 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 46
ID ADC67773 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 47
ID ADC41093 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 48
ID ADC67148 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 49
ID ADC62084 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 50
ID ADC41717 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 51
ID ADC78883 standard; protein; 321 AA.
DE Human PRO protein #56.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

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Query Match      80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity    100.0%; Pred. No. 4.3e-137;
RESULT 52
ID ADE49086 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      80.5%; Score 1688; DB 7; Length 321;
  Best Local Similarity    100.0%; Pred. No. 4.3e-137;
  RESULT 53
  ID ADE35140 standard; protein; 321 AA.
  DE Human secreted/transmembrane protein, PRO362.
  PN US2003203434-A1.
  PD 30-OCT-2003.
  PA (GETH ) GENENTECH INC.
    Query Match      80.5%; Score 1688; DB 7; Length 321;
    Best Local Similarity    100.0%; Pred. No. 4.3e-137;
    RESULT 54
    ID ADE16254 standard; protein; 321 AA.
    DE Human secreted/transmembrane protein, PRO362.
    PN US2003203435-A1.
    PD 30-OCT-2003.
    PA (GETH ) GENENTECH INC.
      Query Match      80.5%; Score 1688; DB 7; Length 321;
      Best Local Similarity    100.0%; Pred. No. 4.3e-137;
      RESULT 55
      ID ADD72869 standard; protein; 321 AA.
      DE Human secreted/transmembrane protein, PRO362.
      PN US2003203436-A1.
      PD 30-OCT-2003.
      PA (GETH ) GENENTECH INC.
        Query Match      80.5%; Score 1688; DB 7; Length 321;
        Best Local Similarity    100.0%; Pred. No. 4.3e-137;
        RESULT 56
        ID ADD72227 standard; protein; 321 AA.
        DE Human secreted/transmembrane protein, PRO362.
        PN US2003194781-A1.
        PD 16-OCT-2003.
        PA (GETH ) GENENTECH INC.
          Query Match      80.5%; Score 1688; DB 7; Length 321;
          Best Local Similarity    100.0%; Pred. No. 4.3e-137;
          RESULT 57
          ID ADE16878 standard; protein; 321 AA.
          DE Human secreted/transmembrane protein, PRO362.
          PN US2003203433-A1.
          PD 30-OCT-2003..
          PA (GETH ) GENENTECH INC.
            Query Match      80.5%; Score 1688; DB 7; Length 321;
            Best Local Similarity    100.0%; Pred. No. 4.3e-137;
            RESULT 58
            ID ADF46892 standard; protein; 321 AA.
            DE Human secreted/transmembrane protein, PRO362.
            PN US2003195333-A1.
            PD 16-OCT-2003.
            PA (GETH ) GENENTECH INC.
              Query Match      80.5%; Score 1688; DB 7; Length 321;
              Best Local Similarity    100.0%; Pred. No. 4.3e-137;
              RESULT 59
              ID ADG52649 standard; protein; 321 AA.
              DE Human secreted/transmembrane protein, PRO362.
              PN US2003216561-A1.
              PD 20-NOV-2003.
              PA (GETH ) GENENTECH INC.
                Query Match      80.5%; Score 1688; DB 7; Length 321;
                Best Local Similarity    100.0%; Pred. No. 4.3e-137;
                RESULT 60
                ID ADG59969 standard; protein; 321 AA.
                DE Human secreted/transmembrane protein, PRO362.
                PN US2003206915-A1.
                PD 06-NOV-2003.
                PA (GETH ) GENENTECH INC.
                  Query Match      80.5%; Score 1688; DB 7; Length 321;
                  Best Local Similarity    100.0%; Pred. No. 4.3e-137;
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Best Local Similarity	100.0%;	Pred. No. 4.3e-137;
RESULT 61		
ID ADH62529 standard; protein; 321 AA.		
DE Human PRO362 protein encoded by DNA45416.		
PN US2003171568-A1.		
PD 11-SEP-2003.		
PA (ASHK/) ASHKENAZI A.		
PA (FONG/) FONG S.		
PA (GODD/) GODDARD A.		
PA (GURN/) GURNEY A L.		
PA (NAPI/) NAPIER M A.		
PA (TUMA/) TUMAS D.		
PA (WOOD/) WOOD W I.		
Query Match	80.5%;	Score 1688; DB 7; Length 321;
Best Local Similarity	100.0%;	Pred. No. 4.3e-137;
RESULT 62		
ID ADI60729 standard; protein; 321 AA.		
DE Human secreted/transmembrane protein, PRO362.		
PN US2003077700-A1.		
PD 24-APR-2003.		
PA (GETH) GENENTECH INC.		
Query Match	80.5%;	Score 1688; DB 7; Length 321;
Best Local Similarity	100.0%;	Pred. No. 4.3e-137;
RESULT 63		
ID ADE48386 standard; protein; 321 AA.		
DE Human secreted/transmembrane protein, PRO362.		
PN US2003104536-A1.		
PD 05-JUN-2003.		
PA (GETH) GENENTECH INC.		
Query Match	80.5%;	Score 1688; DB 8; Length 321;
Best Local Similarity	100.0%;	Pred. No. 4.3e-137;
RESULT 64		
ID ADE89487 standard; protein; 321 AA.		
DE Human secreted/transmembrane protein, PRO362.		
PN US2003130181-A1.		
PD 10-JUL-2003.		
PA (ASHK/) ASHKENAZI A J.		
PA (BAKE/) BAKER K P.		
PA (BOTS/) BOTSTEIN D.		
PA (DESN/) DESNOYERS L.		
PA (EATO/) EATON D L.		
PA (FERR/) FERRARA N.		
PA (FILV/) FILVROFF E.		
PA (FONG/) FONG S.		
PA (GAOW/) GAO W.		
PA (GERB/) GERBER H.		
PA (GERR/) GERRITSEN M E.		
PA (GODD/) GODDARD A.		
PA (GODO/) GODOWSKI P J.		
PA (GIRM/) GIRMALDI J C.		
PA (GURN/) GURNEY A L.		
PA (HILL/) HILLAN K J.		
PA (KLJA/) KLUJAVIN I J.		
PA (KUOS/) KUO S S.		
PA (NAPI/) NAPIER M A.		
PA (PANJ/) PAN J.		
PA (PAON/) PAONI N F.		
PA (ROYM/) ROY M A.		
PA (SHEL/) SHELTON D L.		
PA (STEW/) STEWART T A.		
PA (TUMA/) TUMAS D.		
PA (WILL/) WILLIAMS P M.		
PA (WOOD/) WOOD W I.		
Query Match	80.5%;	Score 1688; DB 8; Length 321;
Best Local Similarity	100.0%;	Pred. No. 4.3e-137;
RESULT 65		
ID ADF61127 standard; protein; 321 AA.		
DE Human secreted/transmembrane protein, PRO362.		
PN US2003195345-A1.		
PD 16-OCT-2003.		
PA (GETH) GENENTECH INC.		
Query Match	80.5%;	Score 1688; DB 8; Length 321;
Best Local Similarity	100.0%;	Pred. No. 4.3e-137;
Best Local Similarity	100.0%;	Pred. No. 4.3e-137;

RESULT 66
ID ADF39819 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 67
ID ADF45615 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 68
ID ADF24011 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 69
ID ADF40443 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 70
ID ADF23387 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 71
ID ADF33370 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 72
ID ADF26837 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 73
ID ADF27473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 74
ID ADF41067 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 75
ID ADF48353 standard; protein; 321 AA.

ID ADF32746 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 76
ID ADF25112 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 77
ID ADF26213 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 78
ID ADF34002 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 79
ID ADF46239 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 80
ID ADG50225 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 81
ID ADG49601 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 82
ID ADG51473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 83
ID ADG48977 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 84
ID ADG48353 standard; protein; 321 AA.

DE Human secreted/transmembrane protein, PRO362.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 85
ID ADG50849 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 86
ID ADG58793 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 87
ID ADG62249 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 88
ID ADH25274 standard; protein; 321 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:52.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 89
ID ADM17051 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 90
ID ADL06885 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 91
ID ADN35285 standard; protein; 321 AA.
DE Human STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 92
ID ADA57531 standard; protein; 305 AA.
DE Human secreted protein #466.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 6.1e-125;
RESULT 93
ID ADA41415 standard; protein; 305 AA.
DE Human secreted protein.

PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 6; Length 305;
Best Local Similarity 76.2%; Pred. No. 6.1e-125;
RESULT 94
ID ABR48114 standard; protein; 305 AA.
DE Human secreted protein, SEQ ID 1005.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 6; Length 305;
Best Local Similarity 76.2%; Pred. No. 6.1e-125;
RESULT 95
ID ABR00282 standard; protein; 305 AA.
DE Human gene 147 encoded secreted protein HSDEK49, SEQ ID NO:571.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 6; Length 305;
Best Local Similarity 76.2%; Pred. No. 6.1e-125;
RESULT 96
ID ADB91804 standard; protein; 305 AA.
DE Human secreted protein #SEQ ID 750.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 7; Length 305;
Best Local Similarity 76.2%; Pred. No. 6.1e-125;
RESULT 97
ID ADC74547 standard; protein; 305 AA.
DE Human secreted protein - SEQ ID 1180.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 7; Length 305;
Best Local Similarity 76.2%; Pred. No. 6.1e-125;
RESULT 98
ID ADN35312 standard; protein; 305 AA.
DE Human short STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 73.7%; Score 1547; DB 8; Length 305;
Best Local Similarity 76.2%; Pred. No. 6.1e-125;
RESULT 99
ID AAY30814 standard; protein; 306 AA.
DE Human secreted protein encoded from gene 4.
PN WO9940100-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 73.7%; Score 1547; DB 2; Length 306;
Best Local Similarity 76.2%; Pred. No. 6.2e-125;
RESULT 100
ID ADL67174 standard; protein; 281 AA.
DE Human B7-H6 (ECD) protein SEQ ID NO:44.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 70.5%; Score 1480; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.4e-119;
RESULT 101
ID AAM93588 standard; protein; 184 AA.
DE Human polypeptide, SEQ ID NO: 3387.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 46.9%; Score 983; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
RESULT 102
ID ADL31354 standard; protein; 184 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3387.
PN EP1396543-A2.

PD 10-MAR-2004;
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 46.9%; Score 983; DB 8; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.6e-76;
RESULT 103
ID AAY82322 standard; protein; 175 AA.
DE Human protein transport molecule (PTAM) SEQ ID NO:6.
PN WO200012703-A2.
PD 09-MAR-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 41.5%; Score 870; DB 3; Length 175;
Best Local Similarity 64.7%; Pred. No. 8.8e-67;
RESULT 104
ID ADK70486 standard; protein; 175 AA.
DE Respiratory disease differentially expressed protein #52.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 41.5%; Score 870; DB 8; Length 175;
Best Local Similarity 64.7%; Pred. No. 8.8e-67;
RESULT 105
ID ADL67144 standard; protein; 280 AA.
DE Mouse B7-H6 protein SEQ ID NO:14.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 40.0%; Score 840; DB 8; Length 280;
Best Local Similarity 47.4%; Pred. No. 6.8e-64;
RESULT 106
ID ADN35313 standard; protein; 280 AA.
DE Murine STIGMA protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 40.0%; Score 840; DB 8; Length 280;
Best Local Similarity 47.4%; Pred. No. 6.8e-64;
RESULT 107
ID ADL67146 standard; protein; 188 AA.
DE Mouse B7-H6 (ECD) protein SEQ ID NO:16.
PN WO2004022594-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match 29.2%; Score 613; DB 8; Length 188;
Best Local Similarity 45.7%; Pred. No. 1.6e-44;
RESULT 108
ID AAE10596 standard; protein; 93 AA.
DE Human macrophage-expressed protein #21.
PN WO200164839-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 23.5%; Score 492; DB 4; Length 93;
Best Local Similarity 98.9%; Pred. No. 1.7e-34;
RESULT 109
ID ADH80723 standard; protein; 300 AA.
DE Human polypeptide #40.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.
PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOU/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match 8.6%; Score 180; DB 8; Length 300;
Best Local Similarity 27.9%; Pred. No. 8.1e-07;
RESULT 110
ID AAY23321 standard; protein; 299 AA.
DE Amino acid sequence of the PRO301 polypeptide.

PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 111
ID AAW74464 standard; protein; 299 AA.
DE F11 antigen protein sequence.
PN WO9902561-A1.
PD 21-JAN-1999.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 8.5%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 112
ID AAY08071 standard; protein; 299 AA.
DE Human PRO307 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 113
ID AAY13364 standard; protein; 299 AA.
DE Amino acid sequence of protein PRO301.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 2; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 114
ID AAY76011 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:189.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 115
ID AAY76076 standard; protein; 299 AA.
DE Human A33 receptor homologue, SEQ ID NO:331.
PN WO9955865-A1.
PD 04-NOV-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 116
ID AAY70670 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 117
ID AAB24405 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:90.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 118
ID AAY95344 standard; protein; 299 AA.
DE Human PRO301 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 119
ID AAB80232 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200104311-A1.

PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 120
ID AAM93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 121
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 122
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 123
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 124
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 125
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 126
ID AAB53086 standard; protein; 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 127
ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 128
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.

PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 129
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 130
ID AAE03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 131
ID AAE03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 132
ID AAE03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 133
ID ABB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 134
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 135
ID ABB64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 136
ID ABB64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 137
ID ABB72215 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.

Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 138
ID ABB72150 standard; protein; 299 AA.
DE Human protein isolated from skin cells SEQ ID NO: 189.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 139
ID ABB95449 standard; protein; 299 AA.
DE Human angiotensin related protein PRO301 SEQ ID NO: 54.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.5%; Score 178.5; DB 5; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 140
ID ABU71610 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 141
ID ABO17798 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 142
ID ABU71465 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 143
ID ABO25173 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 144
ID ABU81052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 145
ID ABU71911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 146
ID ABO01794 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 147
ID ABU66752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 148
ID ABU54367 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 149
ID ABU67291 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 150
ID ABO47382 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 151
ID ABU59833 standard; protein; 299 AA.
DE Novel secreted and transmembrane protein PRO301.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 152
ID ABO25023 standard; protein; 299 AA.
DE Human secreted/transmembrane protein (PRO) #183.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 153
ID ABU64519 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #23.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 154

ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 155
ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 156
ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 157
ID ABO1485 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 158
ID ABU07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 159
ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (hujam1).
PN WO2003008541-A2.
PD 30-JAN-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 160
ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 161
ID ABU69642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 162
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 163
ID ABO14824 standard; protein; 299 AA.

DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 164
ID ADA45885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 165
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 166
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 167
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 168
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 169
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 170
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 171
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 172
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 173
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 174
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 175
ID ABO32776 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 176
ID ADA67539 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 177
ID ADB30546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 178
ID ADA85842 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 179
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 180
ID ADA79358 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 181
ID ADA87497 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087345-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 182
ID ADB16699 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 183
ID ABO34836 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 184
ID ADA16155 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 185
ID ADA91791 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 186
ID ADB14854 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 187
ID ADA47263 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 188
ID ADB18815 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 189
ID ADA94030 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 190
ID ADB19926 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082691-A1.
PD 01-MAY-2003.

PA	(GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	Length 299;
Query Match					
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 191					
ID	ADB13238 standard; protein; 299 AA.				
DE	Human PRO polypeptide #183.				
PN	US2003082710-A1.				
PD	01-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 192					
ID	ABO43331 standard; protein; 299 AA.				
DE	Novel human secreted and transmembrane protein PRO301.				
PN	US2003044945-A1.				
PD	06-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 193					
ID	ADA74492 standard; protein; 299 AA.				
DE	Human PRO polypeptide #183.				
PN	US2003068798-A1.				
PD	10-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 194					
ID	ADA42300 standard; protein; 299 AA.				
DE	Human secreted/transmembrane protein, #25.				
PN	US2003054401-A1.				
PD	20-MAR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 195					
ID	ADB24725 standard; protein; 299 AA.				
DE	Human PRO polypeptide SEQ ID NO 366.				
PN	US2003077713-A1.				
PD	24-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 196					
ID	ADA82249 standard; protein; 299 AA.				
DE	Human PRO polypeptide #183.				
PN	US2003082701-A1.				
PD	01-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 197					
ID	ADA75212 standard; protein; 299 AA.				
DE	Human PRO polypeptide #183.				
PN	US2003073216-A1.				
PD	17-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 198					
ID	ADA85290 standard; protein; 299 AA.				
DE	Novel human secreted and transmembrane protein PRO301.				
PN	US2003082695-A1.				
PD	01-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 199					
ID	ADA84738 standard; protein; 299 AA.				
DE	Novel human secreted and transmembrane protein PRO301.				
PN	US2003082708-A1.				
PD	01-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		8.5%;	Score 178.5;	DB 6;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;			
RESULT 199					
ID	ADA84738 standard; protein; 299 AA.				
DE	Novel human secreted and transmembrane protein PRO301.				
PN	US2003082708-A1.				
PD	01-MAY-2003.				
PA	(GETH) GENENTECH INC.				

Query Match	8.5%;	Score 178.5;	DB 6;	length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 200				
ID ABO17514 standard; protein;	299 AA.			
DE Human PRO polypeptide #21.				
PN US2003064367-A1.				
PD 03-APR-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 201				
ID ADB29994 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003073214-A1.				
PD 17-APR-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 202				
ID ADA80522 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003082761-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 203				
ID ADA75764 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003082703-A1.				
PD 01-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 204				
ID ADA46989 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003073210-A1.				
PD 17-APR-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 205				
ID ADB25285 standard; protein;	299 AA.			
DE Human PRO polypeptide SEQ ID NO 366.				
PN US2003077715-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 206				
ID ADA93461 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003077721-A1.				
PD 24-APR-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 207				
ID ADB26811 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003092147-A1.				
PD 15-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 208				
ID ADB31098 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003096386-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 209				
ID ADB31098 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003096386-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 210				
ID ADB31098 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003096386-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 211				
ID ADB31098 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003096386-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 212				
ID ADB31098 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003096386-A1.				
PD 22-MAY-2003.				
PA (GETH) GENENTECH INC.	8.5%;	Score 178.5;	DB 6;	length 299;
Query Match				


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ID ADB29019 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 228
ID ADA76971 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 229
ID ADA88601 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 230
ID ADA97606 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 231
ID ADB27363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 232
ID ADB22296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 233
ID ABO19860 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO302.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 234
ID ABO17575 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 235
ID ADA66987 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 236
ID ADB22848 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 237
ID ADB23621 standard; protein; 299 AA.
DE Human PRO polypeptide SEQ ID NO 366.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 238
ID ADA92343 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 239
ID ADB15406 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 240
ID ADB38658 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 241
ID ADB38106 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 242
ID ADB66578 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 243
ID ADB89658 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 244
ID ADB90390 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 245
ID ADB77645 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077654-A1.
PD 24-APR-2003.
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Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 264
ID ADC40736 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 265
ID ADC19393 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 266
ID ADC33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 267
ID ADC12911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 268
ID ADC50407 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 269
ID ADC71954 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 270
ID ADC59933 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 271
ID ADC52940 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 272
ID ADC57294 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
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RESULT 273
ID ADC60485 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 274
ID ADC50960 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 275
ID ADC65487 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 276
ID ADC54585 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 277
ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 278
ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 279
ID ADC5947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 280
ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 281
ID ADC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 282
```


ID ADD03191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 283
ID ADC90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 284
ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 285
ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 286
ID ADD10020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 287
ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 288
ID ADC80551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 289
ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 290
ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 291
ID ADC47939 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 292
ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 293
ID ADC79999 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 294
ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 295
ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 296
ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 297
ID ADD03500 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 298
ID ADD41181 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 299
ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 300
ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 301
ID ADD53612 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 302
ID ADD37096 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 303
ID ADD51768 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 304
ID ADD02567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 305
ID ADD02001 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 306
ID ADD54183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 307
ID ADD92500 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 308
ID ADD91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 309
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.

PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 310
ID ADE32307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 311
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 312
ID ADD79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 313
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 314
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 315
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 316
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 317
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 318
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 06-NOV-2003.

[illegible]

Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 328				
ID ADE42551 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003199032-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 329				
ID ADB80567 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003207418-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 330				
ID ADB89595 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003199028-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 331				
ID ADE40879 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003199031-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 332				
ID ADE04678 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003199034-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 333				
ID ADE92807 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003194777-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 334				
ID ADG21516 standard; protein;	299 AA.			
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003207355-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 335				
ID ADG23157 standard; protein;	299 AA.			
DE Novel human secreted and transmembrane protein PRO301.				
PN US2003207384-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
RESULT 336				
ID ADF97492 standard; protein;	299 AA.			
DE Human PRO polypeptide #183.				
PN US2003207370-A1.				
PD 06-NOV-2003.				
PA (GETH) GENENTECH INC.				
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;
Best Local Similarity	26.5%;	Pred. No. 1.1e-06;		
Query Match	8.5%;	Score 178.5;	DB 7;	Length 299;

Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 337
ID ADG80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 338
ID ADG80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 339
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 340
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 341
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 342
ID ADH55296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 343
ID ADH55848 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 344
ID ADI38014 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 345
ID ADI64067 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 346
ID ADI65016 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 347
ID ADI63515 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 348
ID ADH81929 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 349
ID ADH81377 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 350
ID ADJ26282 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 351
ID ADM82546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 352
ID ADN15945 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 353
ID ADN16574 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 354
ID ADN15393 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

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PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 355
ID ADN14841 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 356
ID ADC8103 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 357
ID ADE79197 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 358
ID ADD76551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 359
ID ADD87915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 360
ID ADD86319 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 361
ID ADE79621 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 362
ID ADE75767 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 363
ID ADE73297 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 364
ID ADE41304 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 365
ID ADE23343 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 366
ID ADE23895 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 367
ID ADE24538 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 368
ID ADD87363 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 369
ID ADE89229 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 370
ID ADE41186 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 371
ID ADE73832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 372
ID ADE18368 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194794-A1.
PD 16-OCT-2003.
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PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 373
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 374
ID ADE99386 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 375
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 376
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 377
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 378
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 379
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 380
ID ADE98505 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 381
ID ADE92255 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.

Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 382
ID ADE90556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 383
ID ADE91703 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 384
ID ADE98932 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 385
ID ADG40402 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 386
ID ADF73796 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 387
ID ADG02282 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 388
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 389
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 390
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ID ADF98044 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 391
ID ADG24261 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 392
ID ADF98615 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 393
ID ADG03446 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 394
ID ADF99167 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 395
ID ADG16752 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 396
ID ADG05211 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 397
ID ADG19478 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 398
ID ADF73372 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 399
ID ADG13315 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 400
ID ADG08372 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 401
ID ADG15542 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 402
ID ADF96940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 403
ID ADG06125 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 404
ID ADG23709 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 405
ID ADG03998 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 406
ID ADG24899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 407
ID ADG07196 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 408
ID ADG07748 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.

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PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 409
ID ADG55243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 410
ID ADG60907 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 411
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 412
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 413
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 414
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 415
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 416
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 417
ID ADG58555 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 418
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 419
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 420
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 421
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 422
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 423
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 424
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 425
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 426
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 427
ID ADG52411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 428
ID ADG54139 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 429
ID ADG81108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 430
ID ADG56347 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 431
ID ADH12613 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 432
ID ADG61459 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 433
ID ADH28546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 434
ID ADG54691 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 435
ID ADG59731 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 436
ID ADH20431 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 437
ID ADH43487 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 438
ID ADH07286 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 439
ID ADH59831 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 440
ID ADH06859 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 441
ID ADI81155 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 442
ID ADI18601 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 443
ID ADI65321 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148419-A1.
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PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 444
ID ADI37584 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 445
ID ADG09898 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 446
ID ADH97380 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 447
ID ADI15369 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 448
ID ADG09246 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 449
ID ADI65748 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 450
ID ADI14701 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 451
ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.5%; Score 178.5; DB 8; Length 299;

Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 452
ID ADI18296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 453
ID ADJ99548 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 454
ID ADL08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 455
ID ADI47176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (MAST-) NASTECH PHARM CO INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 456
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 457
ID ADK40844 standard; protein; 299 AA.
DE Human platelet F11 receptor #1.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UNYV) UNIV NEW YORK STATE RES FOUND.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 458
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 459
ID ADM29832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 460
ID ADL77818 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 8.5%; Score 178.5; DB 8; Length 299;

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Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 461
ID ADL77819 standard; protein; 299 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 462
ID ADJ77472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 463
ID ADK82832 standard; protein; 299 AA.
DE Human PRO polypeptide #27.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 464
ID ADJ65594 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 465
ID ADL31332 standard; protein; 299 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3365.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 466
ID ADM27730 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 467
ID ADL26800 standard; protein; 299 AA.
DE Human JAM1 protein SEQ ID NO:54.
PN WO2004022778-A1.
PD 18-MAR-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 468
ID ADM42454 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 469
ID ADO06154 standard; protein; 299 AA.
DE Human PRO polypeptide #21.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 470
ID ADN35284 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 471
ID ADN05140 standard; protein; 299 AA.
DE Antipsoriatic protein sequence #749.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 472
ID ADM28316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 473
ID ADQ95890 standard; protein; 299 AA.
DE T cell activation associated protein #34.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 474
ID ADR11006 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 475
ID ADR17915 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 476
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ID ADR27641 standard; protein; 299 AA.
DE Human F11 receptor protein Seq 7.
PN WO2004063327-A2.
PD 29-JUL-2004.
PA (KORN/) KORNECKI E.
PA (BABI/) BABINSKA A.
PA (EHRL/) EHRLICH Y H.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 477
ID ADI95798 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 478
ID ADI96350 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 479
ID ADR46577 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4, SEQ ID 8.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 480
ID ADR46571 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 481
ID ADR46573 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 482
ID ADR46579 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 5.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 483
ID ADT03591 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 484
ID ADT94260 standard; protein; 299 AA.
DE Human PRO301 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 485
ID ADS74554 standard; protein; 299 AA.
DE Human secreted/transmembrane protein #25.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 486
ID ADE09073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 7; Length 320;
Best Local Similarity 26.5%; Pred. No. 1.2e-06;
RESULT 487
ID ADJ67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 8.5%; Score 178.5; DB 8; Length 335;
Best Local Similarity 26.5%; Pred. No. 1.3e-06;
RESULT 488
ID ADE08038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 7; Length 336;
Best Local Similarity 26.5%; Pred. No. 1.3e-06;
RESULT 489
ID ADQ8964 standard; protein; 34350 AA.
DE Antagonist of cell cycle progression polypeptide #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 8.5%; Score 178; DB 8; Length 34350;
Best Local Similarity 24.2%; Pred. No. 0.0011;
RESULT 490
ID AAW14146 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 8.4%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 491
ID AAY23323 standard; protein; 319 AA.

DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 492
ID AAB65863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.4%; Score 177; DB 4; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 493
ID ADA10947 standard; protein; 319 AA.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US2002160383-A1.
PD 31-OCT-2002.
PA (LASE/) LASHK A W.
PA (JONE/) JONHS D A.
Query Match 8.4%; Score 177; DB 6; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 494
ID ADH62553 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 8.4%; Score 177; DB 7; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 495
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.4%; Score 177; DB 7; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 496
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 177; DB 8; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 497
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO:563.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 177; DB 8; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;
RESULT 498
ID ABP62881 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 8.4%; Score 177; DB 5; Length 336;
Best Local Similarity 27.5%; Pred. No. 1.7e-06;
RESULT 499
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015796-A2.

PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 176.5; DB 3; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.6e-06;
RESULT 500
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 176; DB 2; Length 268;
Best Local Similarity 27.7%; Pred. No. 1.5e-06;
RESULT 501
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 8.4%; Score 176; DB 7; Length 268;
Best Local Similarity 27.7%; Pred. No. 1.5e-06;
RESULT 502
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 176; DB 2; Length 270;
Best Local Similarity 27.7%; Pred. No. 1.5e-06;
RESULT 503
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 176; DB 2; Length 273;
Best Local Similarity 27.7%; Pred. No. 1.6e-06;
RESULT 504
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 8.4%; Score 176; DB 2; Length 273;
Best Local Similarity 27.7%; Pred. No. 1.6e-06;
RESULT 505
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 8.4%; Score 176; DB 7; Length 273;
Best Local Similarity 27.7%; Pred. No. 1.6e-06;
RESULT 506
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.

PA (QIAN/) QIAN X B.
PA (WANG/) WANG Z W.
PA (WEHR/) WEHRMAN T.
PA (ZHAN/) ZHANG J.
PA (ZHOU/) ZHOU P.
PA (CAOY/) CAO Y.
PA (DRMA/) DRMANAC R T.
Query Match
Best Local Similarity 8.3%; Score 173.5; DB 8; Length 301;
Pred. No. 3e-06;
RESULT 507
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 8.2%; Score 172.5; DB 8; Length 316;
Pred. No. 3.9e-06;
RESULT 508
ID AAY23326 standard; protein; 260 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 8.1%; Score 169.5; DB 2; Length 260;
Pred. No. 5.3e-06;
RESULT 509
ID AAY08072 standard; protein; 260 AA.
DE Human DNA40628 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 8.1%; Score 169.5; DB 2; Length 260;
Pred. No. 5.3e-06;
RESULT 510
ID ADH62550 standard; protein; 260 AA.
DE Human PRO301 protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 8.1%; Score 169.5; DB 7; Length 260;
Pred. No. 5.3e-06;
RESULT 511
ID AAY23328 standard; protein; 263 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 8.1%; Score 169.5; DB 2; Length 263;
Pred. No. 5.4e-06;
RESULT 512
ID AAY08074 standard; protein; 263 AA.
DE Human DNA40628 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 8.1%; Score 169.5; DB 2; Length 263;
Pred. No. 5.4e-06;
RESULT 513
ID ADH62552 standard; protein; 263 AA.
DE Human PRO301 protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (WOOD/) WOOD W I.

PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 8.1%; Score 169.5; DB 7; Length 263;
Pred. No. 5.4e-06;
RESULT 514
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIUTTSU SH.
Query Match
Best Local Similarity 8.0%; Score 168; DB 8; Length 300;
Pred. No. 8.8e-06;
RESULT 515
ID AAW61379 standard; protein; 298 AA.
DE Human junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 8.0%; Score 167; DB 2; Length 298;
Pred. No. 1.1e-05;
RESULT 516
ID AAW61380 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule protein.
PN WO9824897-A1.
PD 11-JUN-1998.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match
Best Local Similarity 8.0%; Score 167; DB 2; Length 300;
Pred. No. 1.1e-05;
RESULT 517
ID AAY23325 standard; protein; 300 AA.
DE A33 related antigen JAM.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 8.0%; Score 167; DB 2; Length 300;
Pred. No. 1.1e-05;
RESULT 518
ID ADH62537 standard; protein; 300 AA.
DE Murine JAM protein used in the exemplification of the invention.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 8.0%; Score 167; DB 7; Length 300;
Pred. No. 1.1e-05;
RESULT 519
ID ADK40853 standard; protein; 300 AA.
DE Mouse junction adhesion molecule (JAM).
PN US6699688-B1.
PD 02-MAR-2004.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
Query Match
Best Local Similarity 8.0%; Score 167; DB 8; Length 300;
Pred. No. 1.1e-05;
RESULT 520
ID ADN35293 standard; protein; 300 AA.
DE Human JAM protein.
PN WO2004031105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 8.0%; Score 167; DB 8; Length 300;
Pred. No. 1.1e-05;
RESULT 521
ID ABB83928 standard; protein; 365 AA.
DE PCAR SEQ ID NO 4.
PN US2002059654-A1.
PD 16-MAY-2002.
PA (BUHL/) BUHLER T.
PA (GADI/) GADIENT R A.

PA (KORN/) KORN R.
PA (MOVV/) MOVVA R.
Query Match 8.0%; Score 167; DB 5; Length 365;
Best Local Similarity 24.1%; Pred. No. 1.4e-05;
RESULT 522
ID ABG74786 standard; protein; 31267 AA.
DE Human RGS11 protein.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 7.8%; Score 164.5; DB 6; Length 31267;
Best Local Similarity 22.3%; Pred. No. 0.014;
RESULT 523
ID AAM14158 standard; protein; 318 AA.
DE Mouse A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 7.8%; Score 164; DB 2; Length 318;
Best Local Similarity 22.2%; Pred. No. 2.1e-05;
RESULT 524
ID ABB83927 standard; protein; 261 AA.
DE C-terminally truncated pCAR SEQ ID NO 2.
PN US2002059654-A1.
PD 16-MAY-2002.
PA (BUHL/) BUHLER T.
PA (GADI/) GADIENT R A.
PA (KORN/) KORN R.
PA (MOVV/) MOVVA R.
Query Match 7.8%; Score 163.5; DB 5; Length 261;
Best Local Similarity 27.7%; Pred. No. 1.8e-05;
RESULT 525
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.6%; Score 160; DB 3; Length 280;
Best Local Similarity 24.7%; Pred. No. 3.9e-05;
RESULT 526
ID AAY72878 standard; protein; 352 AA.
DE Human PRO5723 protein encoded by DNA82361 cDNA clone.
PN WO200116319-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 4; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 527
ID AAB50930 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 4; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 528
ID AAB65294 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:505.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 4; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 529
ID ABB84956 standard; protein; 352 AA.
DE Human PRO5723 protein sequence SEQ ID NO:280.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 5; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 530
ID ABB95562 standard; protein; 352 AA.

DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEX A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.6%; Score 159; DB 5; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 531
ID ABU58109 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 532
ID ABU59187 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO5723.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 533
ID ABU82699 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 534
ID ABU60618 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 535
ID ABU80846 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 536
ID ABO33812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 537
ID ABU14000 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.


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Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 538
ID ABU72585 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 539
ID ABG74762 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2002192752-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 540
ID ABU59334 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 541
ID ABO26031 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 542
ID ABU82155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 543
ID ABU59040 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 544
ID ABU92418 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 545
ID ABU59483 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO3301.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 546
ID ABU92249 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 547
ID ABU10955 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 548
ID ABU81707 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 549
ID ABU88646 standard; protein; 352 AA.
DE Human secreted and transmembrane polypeptide PRO5723.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 550
ID ABO34160 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 551
ID ABJ72335 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 552
ID ADA38016 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 553
ID ADA21702 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 554
ID ADA10489 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO5723.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 555
ID ADA18033 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 556
ID ADA28141 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match                                7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 557
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ID ADA94721 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 558
ID ADA38946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 559
ID ABJ72463 standard; protein; 352 AA.
DE Human PRO5743 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 560
ID ADA93067 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 561
ID ABO34358 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO 5723.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 6; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 562
ID ABO53246 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 563
ID ADA22628 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 564
ID ABO22616 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 565
ID ADA06794 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #141.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 566
ID ABJ72165 standard; protein; 352 AA.
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 567

ID ADA39487 standard; protein; 352 AA.
DE Human, secreted/transmembrane protein PRO5723.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 568
ID ADB83706 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 569
ID ADB80812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 570
ID ADB73353 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 571
ID ADB96513 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 572
ID ADB78435 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 573
ID ADB85083 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 574
ID ADB78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 575
ID ADB87255 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 576
ID ADB84837 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003092890-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 577
ID ADB83952 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 578
ID ADB73107 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 579
ID ADC57985 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 580
ID ADC55349 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 581
ID ADC12216 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 582
ID ADC56638 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 583
ID ADC11683 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 584
ID ADC36945 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 585
ID ADC21935 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 586
ID ADC49966 standard; protein; 352 AA.

DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 587
ID ADC49165 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 588
ID ADC49682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 589
ID ADC47543 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 590
ID ADC14805 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 591
ID ADC47288 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 592
ID ADD08337 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 593
ID ADC82162 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 594
ID ADD07804 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 595
ID ADC78163 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.


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Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 596
ID  ADC82695 standard; protein; 352 AA.
DE  Human PRO polypeptide #141.
PN  US2003059833-A1.
PD  27-MAR-2003.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 597
ID  ADD06398 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003073816-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 598
ID  ADD10569 standard; protein; 352 AA.
DE  Human secreted/transmembrane PRO polypeptide #140.
PN  US2003105011-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 599
ID  ADD08875 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003073090-A1.
PD  17-APR-2003.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 600
ID  ADC77917 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003088066-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 601
ID  ADD07124 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2002193300-A1.
PD  19-DEC-2002.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 602
ID  ADD11529 standard; protein; 352 AA.
DE  Human secreted/transmembrane PRO polypeptide #140.
PN  US2003105013-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 603
ID  ADC83371 standard; protein; 352 AA.
DE  Human PRO polypeptide #141.
PN  US2003059783-A1.
PD  27-MAR-2003.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 604
ID  ADD50880 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003105291-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 605
ID  ADD15380 standard; protein; 352 AA.

DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003059437-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 606
ID  ADD51126 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003105290-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 607
ID  ADD55478 standard; protein; 352 AA.
DE  Human PRO polypeptide #141.
PN  US2003077593-A1.
PD  24-APR-2003.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 608
ID  ADD37322 standard; protein; 352 AA.
DE  Human secreted/transmembrane PRO polypeptide #140.
PN  US2003105012-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 609
ID  ADD56436 standard; protein; 352 AA.
DE  Human PRO polypeptide #141.
PN  US2003077594-A1.
PD  24-APR-2003.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 610
ID  ADD50607 standard; protein; 352 AA.
DE  Human PRO polypeptide #108.
PN  US2003096971-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 611
ID  ADD54874 standard; protein; 352 AA.
DE  Human PRO polypeptide #141.
PN  US2002132253-A1.
PD  19-SEP-2002.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 612
ID  ADD50361 standard; protein; 352 AA.
DE  Human PRO polypeptide #108.
PN  US2003096970-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 613
ID  ADD51372 standard; protein; 352 AA.
DE  Novel human secreted and transmembrane protein PRO5723.
PN  US2003105289-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match          7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 614
ID  ADE31893 standard; protein; 352 AA.
DE  Human secreted/transmembrane protein PRO5723.
PN  US2003068647-A1.
PD  10-APR-2003.
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Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 615
ID ADE27028 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 616
ID ADE26495 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 617
ID ADF67432 standard; protein; 352 AA.
DE Human PRO5723 amino acid sequence SEQ ID NO:505.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 618
ID ADE94085 standard; protein; 352 AA.
DE Immune disease treatment/diagnosis related PRO5723.
PN US2003082199-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 619
ID ADI35686 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 620
ID ADI00179 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match                               7.6%; Score 159; DB 7; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 621
ID ADC48919 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 622
ID ADE21090 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 623
ID ADE05934 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 624
ID ADD75163 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 625
ID ADD75909 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 626
ID ADD85141 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 627
ID ADD86967 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 628
ID ADE20844 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 629
ID ADE39141 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 630
ID ADE05688 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 631
ID ADD73673 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 632
ID ADD78513 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match                               7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 633
ID ADE41530 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003100497-A1.
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PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 634
ID ADE21336 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 635
ID ADD77451 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 636
ID ADE20598 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 637
ID ADD75663 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 638
ID ADD74179 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 639
ID ADD74425 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 640
ID ADD76155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 641
ID ADD85647 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 642
ID ADE05196 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 643
ID ADD75409 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 644
ID ADD76953 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 645
ID ADD86721 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 646
ID ADD78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 647
ID ADD77697 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 648
ID ADD77943 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 649
ID ADD85401 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 650
ID ADD73933 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 651
ID ADD74671 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 652
ID ADD77199 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Pred. No. 6.6e-05; Length 352;
RESULT 653
ID ADD85893 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 654
ID ADE05442 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 655
ID ADD74917 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 656
ID ADF35631 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 657
ID ADG11881 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 658
ID ADG05729 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 659
ID ADG27283 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 660
ID ADG11346 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 661
ID ADG12125 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 662
ID ADF94682 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 663
ID ADG06778 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 664
ID ADH39122 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 665
ID ADH19751 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 666
ID ADH21244 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 667
ID ADH20284 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 668
ID ADH43713 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 669
ID ADG34212 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.2%; Score 159; DB 8; Length 352;
RESULT 670
ID ADI33682 standard; protein; 352 AA.
```

DE Human PRO polypeptide #108.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 671
ID ADH69776 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 672
ID ADI29937 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 673
ID ADM27334 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 674
ID ADK83058 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 675
ID ADK66692 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;
RESULT 676
ID AAW69697 standard; protein; 365 AA.
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 7.6%; Score 159; DB 2; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 677
ID AAW57212 standard; protein; 365 AA.
DE Human coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARNER CANCER INST INC.
Query Match 7.6%; Score 159; DB 2; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 678
ID AAB47270 standard; protein; 365 AA.
DE Human CAR.
PN US6245966-B1.
PD 12-JUN-2001.
PA (UYTE-) UNIV TECHNOLOGY CORP.
Query Match 7.6%; Score 159; DB 4; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 679
ID ABB08040 standard; protein; 365 AA.
DE Human coxsackie-adenovirus receptor (CAR).

PN WO200229072-A2.
PD 11-APR-2002.
PA (NOVS) NOVARTIS AG.
Query Match 7.6%; Score 159; DB 5; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 680
ID ABJ37063 standard; protein; 365 AA.
DE Human breast cancer / ovarian cancer related protein #39.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.6%; Score 159; DB 6; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 681
ID ADB97544 standard; protein; 365 AA.
DE Human CAR wild-type protein.
PN WO2003070915-A2.
PD 28-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 7.6%; Score 159; DB 7; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 682
ID ADN95226 standard; protein; 365 AA.
DE Human BEC/LEC-related protein sequence SegID148.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.6%; Score 159; DB 7; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;
RESULT 683
ID ABU12046 standard; protein; 505 AA.
DE Human NOV4a CG59871-01 protein SEQ ID 12.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.6%; Score 159; DB 6; Length 505;
Best Local Similarity 23.2%; Pred. No. 0.00011;
RESULT 684
ID AAY41692 standard; protein; 373 AA.
DE Human PRO 363 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 2; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 685
ID AAB33430 standard; protein; 373 AA.
DE Human PRO363 protein UNQ318 SEQ ID NO:87.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 3; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 686
ID AAB44248 standard; protein; 373 AA.
DE Human PRO363 (UNQ318) protein sequence SEQ ID NO:59.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 3; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 687
ID AAU12365 standard; protein; 373 AA.
DE Human PRO363 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 688
ID AAB48146 standard; protein; 373 AA.

DE Human A236 variant 2 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 689
ID AAB48108 standard; protein; 373 AA.
DE Human A236 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 690
ID AAB65293 standard; protein; 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:503.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 691
ID AAU83656 standard; protein; 373 AA.
DE Human PRO protein, Seq ID No 130.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 692
ID ABB84848 standard; protein; 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:64.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 693
ID AAE26448 standard; protein; 373 AA.
DE Human A236 protein.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 694
ID ABB95454 standard; protein; 373 AA.
DE Human angiotensin related protein PRO363 SEQ ID NO: 64.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODO/) GODDARD A.
PA (GODO/) GODDARD P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 695
ID ABU58108 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 696
ID ABU59186 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO363.
PN US200213252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 697
ID ABU82698 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003032023-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 698
ID ABO17809 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 699
ID ABU60617 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 700
ID ABU80803 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 701
ID ABO25194 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 702
ID ABO33769 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 703
ID ABU13999 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.

Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 704				
ID ABU81063 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003004311-A1.				
PD 02-JAN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 705				
ID ABU72200 standard; protein; 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2002192706-A1.				
PD 19-DEC-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 706				
ID ABU72584 standard; protein; 373 AA.				
DE Novel human secreted and transmembrane protein PRO363.				
PN US2003003531-A1.				
PD 02-JAN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 707				
ID ABU66763 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003036180-A1.				
PD 20-FEB-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 708				
ID ABU84880 standard; protein; 373 AA.				
DE Human secreted and transmembrane polypeptide PRO363.				
PN US2002177553-A1.				
PD 28-NOV-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 709				
ID ABUS9844 standard; protein; 373 AA.				
DE Novel secreted and transmembrane protein PRO363.				
PN US2003017563-A1.				
PD 23-JAN-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 710				
ID ABU61078 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2002169284-A1.				
PD 14-NOV-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 711				
ID ABUS9333 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, #176.				
PN US2003027162-A1.				
PD 06-FEB-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 712				
ID ABO26030 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2002127576-A1.				
PD 12-SEP-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 713				
ID ABO26030 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2002127576-A1.				
PD 12-SEP-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 714				
ID ABO26030 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2002127576-A1.				
PD 12-SEP-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 715				
ID ABO26030 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2002127576-A1.				
PD 12-SEP-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 716				
ID ABO26030 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2002127576-A1.				
PD 12-SEP-2002.				
PA (GETH) GENENTECH INC.				
Query Match	7			

RESULT 713	ID	ABO25034 standard; protein; 373 AA.			
	DE	Human secreted/transmembrane protein (PRO) #194.			
	PN	US2003036179-A1.			
	PD	20-FEB-2003.			
	PA	(GETH) GENENTECH INC.			
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 714	ID	ABU80347 standard; protein; 373 AA.		
		DE	Human secreted/transmembrane protein PRO363.		
		PN	US2003004102-A1.		
		PD	02-JAN-2003.		
		PA	(GETH) GENENTECH INC.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 715	ID	ABU82112 standard; protein; 373 AA.		
		DE	Novel human secreted and transmembrane protein PRO363.		
		PN	US2003088063-A1.		
		PD	08-MAY-2003.		
		PA	(GETH) GENENTECH INC.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 716	ID	ABU59039 standard; protein; 373 AA.		
		DE	Human secreted/transmembrane protein, #176.		
		PN	US2002142961-A1.		
		PD	03-OCT-2002.		
		PA	(GETH) GENENTECH INC.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 717	ID	ABU92417 standard; protein; 373 AA.		
		DE	Novel human secreted and transmembrane protein PRO363.		
		PN	US2003022187-A1.		
		PD	30-JAN-2003.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 718	ID	ABU59482 standard; protein; 373 AA.		
		DE	Novel human secreted or transmembrane protein PRO5723.		
		PN	US2003027985-A1.		
		PD	06-FEB-2003.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 719	ID	ABU67039 standard; protein; 373 AA.		
		DE	Human secreted/transmembrane, PRO, protein SEQ ID 388.		
		PN	US2003032155-A1.		
		PD	13-FEB-2003.		
		PA	(GETH) GENENTECH INC.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 720	ID	ABU92248 standard; protein; 373 AA.		
		DE	Novel human secreted and transmembrane protein PRO363.		
		PN	US2003017476-A1.		
		PD	23-JAN-2003.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 721	ID	ABU10954 standard; protein; 373 AA.		
		DE	Human PRO polypeptide #140.		
		PN	US2002123463-A1.		
		PD	05-SEP-2002.		
		PA	(GETH) GENENTECH INC.		
	Query Match	7.6%;	Score 158.5;	DB 6;	Length 373;
	Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
	RESULT 722	ID	ABU81706 standard; protein; 373 AA.		
		DE	Novel human secreted and transmembrane protein PRO363.		
		PN	US2002177164-A1.		

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PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 723
ID ABU88645 standard; protein; 373 AA.
DE Human secreted and transmembrane polypeptide PRO363.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 724
ID ABO34159 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 725
ID ADA45907 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 726
ID ADA76338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 727
ID ABJ72292 standard; protein; 373 AA.
DE Human PRO363 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 728
ID ADA18988 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 729
ID ADA61611 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 730
ID ADB19396 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 731
ID ADB27937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 732
ID ADA86416 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 733
ID ADB15980 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 734
ID ADA38014 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 735
ID ADA47766 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 736
ID ADA21700 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 737
ID ADA10487 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 738
ID ADA67561 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 739
ID ADB30568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 740
ID ADA85864 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e-05; Length 373;
RESULT 741
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ID ADA18031 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 742
ID ADA97076 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 743
ID ADA79380 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 744
ID ADA87519 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 745
ID ADB16721 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 746
ID ADA28139 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 747
ID ADA91813 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 748
ID ADB14876 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 749
ID ADA24598 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 750
ID ADB18837 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073211-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 751
ID ADA94052 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 752
ID ADB19948 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 753
ID ADB13260 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 754
ID ABO43342 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 755
ID ABO19649 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 756
ID ADA12259 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 757
ID ADA94719 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 758
ID ADA74514 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 759
ID ADB24747 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 760
ID ADA82271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 761
ID ADA75234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 762
ID ADA85312 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 763
ID ADA84760 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 764
ID ADB30016 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 765
ID ADA80544 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 766
ID ADA75786 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 767
ID ADA38944 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 768
ID ADA47011 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 769
ID ADB25307 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 770
ID ADA93483 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 771
ID ADB26833 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 772
ID ADB31120 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 773
ID ABJ72420 standard; protein; 373 AA.
DE Human PRO363 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 774
ID ADA93065 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 775
ID ADA61048 standard; protein; 373 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 776
ID ADB24195 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 777
ID ADA96524 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 778
ID ADA81096 standard; protein; 373 AA.

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DE Human PRO polypeptide #194.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 779
ID ADA95972 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 780
ID ADB26281 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 781
ID ADB21766 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 782
ID ABO34315 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO 363.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 783
ID ABO19540 standard; protein; 373 AA.
DE Novel human secreted and transmembrane polypeptide #8.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 784
ID ADA77545 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 785
ID ADB18285 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 786
ID ADA86968 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 787
ID ADA88071 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 788
ID ADA46459 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 789
ID ADB28489 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 790
ID ADB29041 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 791
ID ABO53245 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 792
ID ADA76993 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 793
ID ADA22626 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 794
ID ADA88623 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 795
ID ADA97628 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 796
ID ADB27385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
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RESULT 797
ID ADB22318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 798
ID ABO22615 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 799
ID ADA06792 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #140.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 800
ID ABJ72122 standard; protein; 373 AA.
DE Human membrane bound receptor/protein PRO363 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 801
ID ADA39485 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 802
ID ADA67009 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 803
ID ADB22870 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 804
ID ADB23643 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 805
ID ADA92365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 806
ID ADB15428 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 807
ID ADB83620 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 808
ID ADB80726 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 809
ID ADB73267 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 810
ID ADB38680 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 811
ID ADB96511 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 812
ID ADB78349 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 813
ID ADB38128 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 814
ID ADB66600 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
RESULT 815
ID ADB84997 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
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Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 816
ID ADB89680 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 817
ID ADB90412 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 818
ID ADB39513 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 819
ID ADB78103 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 820
ID ADB73565 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 821
ID ADB87169 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 822
ID ADB84751 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 823
ID ADB47136 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 824
ID ADB83866 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 825
ID ADB86743 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 826
ID ADB73021 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 827
ID ADB76281 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 828
ID ADB77348 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 829
ID ADB34505 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 830
ID ADB35609 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 831
ID ADB33953 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 832
ID ADB35057 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 833
ID ADB36161 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 834

ID ADB46556 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 835
ID ADC43707 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 836
ID ADC57983 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 837
ID ADC55347 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 838
ID ADC12214 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 839
ID ADC61467 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 840
ID ADC63431 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 841
ID ADC66531 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 842
ID ADC56636 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 843
ID ADC68655 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 844
ID ADC62715 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 845
ID ADC67780 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 846
ID ADC11681 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 847
ID ADC41100 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 848
ID ADC67155 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 849
ID ADC62091 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 850
ID ADC36859 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 851
ID ADC41724 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 852
ID ADC21849 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

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RESULT 853
ID ADC50429 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 854
ID ADC71976 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 855
ID ADC59955 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 856
ID ADC49880 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 857
ID ADC49079 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 858
ID ADC49596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 859
ID ADC47457 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 860
ID ADC52962 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 861
ID ADC57316 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 862
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ID ADC60507 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 863
ID ADC50982 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 864
ID ADC65509 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 865
ID ADC54607 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 866
ID ADC53568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 867
ID ADC59091 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 868
ID ADC55969 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 869
ID ADC58539 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 870
ID ADC14803 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 871
ID ADC47202 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
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PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 872
ID ADD08335 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 873
ID ADD03213 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 874
ID ADC90205 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 875
ID ADC82160 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 876
ID ADC69624 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 877
ID ADC48513 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 878
ID ADD10042 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 879
ID ADD07802 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 880
ID ADC7807 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 881
ID ADD04617 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 882
ID ADC82693 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 883
ID ADD06312 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 884
ID ADC80573 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 885
ID ADD11080 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 886
ID ADD10353 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 887
ID ADC47961 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 888
ID ADD08673 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 889
ID ADC77831 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 890
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ID ADC80021 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 891
ID ADD07122 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 892
ID ADD11313 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 893
ID ADD09490 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 894
ID ADC83369 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 895
ID ADD50794 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 896
ID ADD41203 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 897
ID ADD52342 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 898
ID ADD51040 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 899
ID ADD53082 standard; protein; 373 AA.
DE Human PRO polypeptide #194.

PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 900
ID ADD53634 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 901
ID ADD5476 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 902
ID ADD37106 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 903
ID ADD56434 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 904
ID ADD51790 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 905
ID ADD02589 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 906
ID ADD50521 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 907
ID ADD02023 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 908
ID ADD54205 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 909
ID ADD54872 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 910
ID ADD50275 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 911
ID ADD51286 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 912
ID ADE49093 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 913
ID ADD92522 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 914
ID ADD91418 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 915
ID ADE04032 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 916
ID ADE31891 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 917
ID ADE27026 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 918

ID ADE32329 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 919
ID ADE22261 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 920
ID ADD79485 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 921
ID ADE35147 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 922
ID ADE16261 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 923
ID ADD72876 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 924
ID ADE42021 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 925
ID ADE17838 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 926
ID ADD91970 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 927
ID ADE33433 standard; protein; 373 AA.


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DE Novel human secreted and transmembrane protein PRO363.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 928
ID ADE33985 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 929
ID ADD80037 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 930
ID ADD93074 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 931
ID ADD72234 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 932
ID ADE19494 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 933
ID ADE18942 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 934
ID ADE43138 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 935
ID ADD95927 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 936
ID ADE22813 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 937
ID ADD78931 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 938
ID ADE26493 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 939
ID ADE32881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 940
ID ADE42573 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 941
ID ADE16885 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 942
ID ADD80589 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 943
ID ADD89617 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 944
ID ADE40901 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 945
ID ADE04700 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
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PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 946
ID ADE92829 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 947
ID ADF46899 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 948
ID ADF67430 standard; protein; 373 AA.
DE Human PRO363; amino acid sequence SEQ ID NO:503.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 949
ID ADG21538 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 950
ID ADG23179 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 951
ID ADF97514 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 952
ID ADG80578 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 953
ID ADG52656 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 954
ID ADG59976 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.

Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 955
ID ADG80026 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 956
ID ADH55318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 957
ID ADH55870 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 958
ID ADI35684 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 959
ID ADI60736 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 960
ID ADI64089 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 961
ID ADI65038 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 962
ID ADI63537 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 963
ID ADH81951 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
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RESULT 964
ID ADI00177 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003049682-A1.
PD 13-MAR-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 965
ID ADH81399 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207377-A1.
PD 06-NOV-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 966
ID ADM82568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087355-A1.
PD 08-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 967
ID ADN15967 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087353-A1.
PD 08-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 968
ID ADN16596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087385-A1.
PD 08-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 969
ID ADN15415 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087356-A1.
PD 08-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 970
ID ADN14863 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087357-A1.
PD 08-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 971
ID ADC48833 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092888-A1.
PD 15-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;
    Pred. No. 7.9e-05;
  RESULT 972
ID ADC81125 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092115-A1.
PD 15-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 973
ID ADE21004 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100735-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 974
ID ADE05848 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100728-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 975
ID ADD76573 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003100087-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 976
ID ADD75077 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100712-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 977
ID ADD75823 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100717-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 978
ID ADD85055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100722-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 979
ID ADD86881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100738-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 980
ID ADE20758 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100734-A1.
PD 29-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 981
ID ADE39055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096362-A1.
PD 22-MAY-2003.
  Query Match
    Best Local Similarity 22.2%; Score 158.5; DB 8; Length 373;
    Pred. No. 7.9e-05;
  RESULT 982
ID ADD87937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
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PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 983
ID ADD86341 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 984
ID ADE05602 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 985
ID ADD73587 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 986
ID ADE75789 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 987
ID ADE48393 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 988
ID ADD78427 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 989
ID ADE41314 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 990
ID ADE23365 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 991
ID ADE21250 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100736-A1.

PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 992
ID ADD77365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 993
ID ADE20512 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 994
ID ADD75577 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 995
ID ADD74093 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 996
ID ADD74339 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 997
ID ADD76069 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 998
ID ADD85561 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 999
ID ADE23917 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1000
ID ADE24560 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003092111-A1.
PD 15-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1001
ID ADD87385 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1002
ID ADE05110 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1003
ID ADD75323 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1004
ID ADD76867 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1005
ID ADD86635 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1006
ID ADE89251 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1007
ID ADD78103 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1008
ID ADE18390 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1009
ID ADE88699 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1010
ID ADE89494 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1011
ID ADD77611 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1012
ID ADD77857 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1013
ID ADD85315 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1014
ID ADD73847 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1015
ID ADD74585 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100713-A1.
PD 29-MAY-2003.
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PA	(GETH) GENENTECH INC.	7.6%;	Score 158.5;	DB 8;	Length 373;
Query Match					
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1016					
ID	ADD7113 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003100716-A1.				
PD	29-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1017					
ID	ADD85807 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003100720-A1.				
PD	29-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1018					
ID	ADE05356 standard; protein; 373 AA.				
DE	Human PRO polypeptide #65.				
PN	US2003100723-A1.				
PD	29-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1019					
ID	ADD74831 standard; protein; 373 AA.				
DE	Human PRO polypeptide #65.				
PN	US2003100724-A1.				
PD	29-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1020					
ID	ADFE1134 standard; protein; 373 AA.				
DE	Human secreted/transmembrane protein, PRO363.				
PN	US2003195345-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1021					
ID	ADFP3826 standard; protein; 373 AA.				
DE	Human secreted/transmembrane protein, PRO363.				
PN	US2003198994-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1022					
ID	ADFA5622 standard; protein; 373 AA.				
DE	Human secreted/transmembrane protein, PRO363.				
PN	US2003195148-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1023					
ID	ADBE94719 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003199027-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1024					
ID	ADBE91130 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003199061-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity		22.2%;	Pred. No. 7.9e-05;		
RESULT 1024					
ID	ADBE91130 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003199061-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				

Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1025				
ID ADF35629 standard; protein; 373 AA.				
DE Human PRO363 polypeptide.				
PN US2003194760-A1.				
PD 16-OCT-2003.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1026				
ID ADE95271 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003199052-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1027				
ID ADE93381 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003199060-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1028				
ID ADF24018 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003204055-A1.				
PD 30-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1029				
ID ADF40450 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199021-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1030				
ID ADF23394 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003203402-A1.				
PD 30-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1031				
ID ADF33377 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003194780-A1.				
PD 16-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1032				
ID ADF34962 standard; protein; 373 AA.				
DE Human PRO polypeptide #194.				
PN US2003199029-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1033				
ID ADF26844 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199436-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1034				
ID ADF26844 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199436-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1035				
ID ADF26844 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199436-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1036				
ID ADF26844 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199436-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;		
RESULT 1037				
ID ADF26844 standard; protein; 373 AA.				
DE Human secreted/transmembrane protein, PRO363.				
PN US2003199436-A1.				
PD 23-OCT-2003.				
PA (GETH) GENENTECH INC.				
Query Match	7.6%;			

RESULT 1034
ID ADF27480 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1035
ID ADE92277 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1036
ID ADE90578 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1037
ID ADF41074 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1038
ID ADF32753 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1039
ID ADF25119 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1040
ID ADF26220 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1041
ID ADF34009 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1042
ID ADF46246 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1043

ID ADE91725 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1044
ID ADG11879 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1045
ID ADG05643 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1046
ID ADG27197 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1047
ID ADG02304 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1048
ID ADG22090 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1049
ID ADG20160 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1050
ID ADF98066 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1051
ID ADG24283 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1052
ID ADF98637 standard; protein; 373 AA.

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DE Human PRO polypeptide #194.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1053
ID ADG03468 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1054
ID ADF99189 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1055
ID ADG16774 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1056
ID ADG05233 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1057
ID ADG19500 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1058
ID ADG11260 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1059
ID ADG13337 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1060
ID ADG08394 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1061
ID ADG15564 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1062
ID ADG12039 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1063
ID ADF96962 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1064
ID ADG06147 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1065
ID ADG23731 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1066
ID ADG04020 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1067
ID ADG24921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1068
ID ADF94596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1069
ID ADG07218 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1070
ID ADG07770 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207356-A1.
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PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1071	
ID	ADG06692 standard; protein; 373 AA.
DE	Human PRO polypeptide #65.
PN	US2003096966-A1.
PD	22-MAY-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1072	
ID	ADG55265 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003194778-A1.
PD	16-OCT-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1073	
ID	ADG60929 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003207390-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1074	
ID	ADG62033 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003207428-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1075	
ID	ADG82234 standard; protein; 373 AA.
DE	Human PRO polypeptide #194.
PN	US2003207358-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1076	
ID	ADG57473 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003207362-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1077	
ID	ADG56921 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003207364-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1078	
ID	ADG55817 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003207365-A1.
PD	06-NOV-2003.
PA	(GETH) GENENTECH INC.
Query Match	7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity	22.2%; Pred. No. 7.9e-05;
RESULT 1079	
ID	ADG58577 standard; protein; 373 AA.
DE	Novel human secreted and transmembrane protein PRO363.
PN	US2003207368-A1.
PD	06-NOV-2003.

PA	(GETH) GENENTECH INC.	7.6%;	Score 158.5;	DB 8;	Length 373;
Query Match					
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1080					
ID	ADG70943 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207420-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1081					
ID	ADH39036 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003096965-A1.				
PD	22-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1082					
ID	ADG58025 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207363-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1083					
ID	ADG53609 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207415-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1084					
ID	ADG71495 standard; protein; 373 AA.				
DE	Novel human secreted and transmembrane protein PRO363.				
PN	US2003207421-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1085					
ID	ADG50232 standard; protein; 373 AA.				
DE	Human secreted/transmembrane protein, PRO363.				
PN	US2003207803-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1086					
ID	ADG81682 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003207805-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1087					
ID	ADH19749 standard; protein; 373 AA.				
DE	Human secreted/transmembrane protein PRO363.				
PN	US2003228656-A1.				
PD	11-DEC-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1088					
ID	ADH30644 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003077723-A1.				
PD	24-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1089					
ID	ADH30644 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003077723-A1.				
PD	24-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1090					
ID	ADH30644 standard; protein; 373 AA.				
DE	Human PRO polypeptide #194.				
PN	US2003077723-A1.				
PD	24-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		7.6%;	Score 158.5;	DB 8;	Length 373;
Best Local Similarity	22.2%;	Pred. No. 7.9e-05;			
RESULT 1091					
ID	ADH30644 standard; protein; 373 AA.				

Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1089
ID ADH12011 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1090
ID ADG49608 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1091
ID ADG51480 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1092
ID ADG52433 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1093
ID ADG54161 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1094
ID ADG48984 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1095
ID ADG81130 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1096
ID ADG56369 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1097
ID ADH12635 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 1098
ID ADG48360 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1099
ID ADH21242 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1100
ID ADG61481 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1101
ID ADH20282 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1102
ID ADH28568 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1103
ID ADG54713 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1104
ID ADG59753 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1105
ID ADG50856 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1106
ID ADH43497 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1107
ID ADG58800 standard; protein; 373 AA.

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DE Human secreted/transmembrane protein, PRO363.
PN US2004005657-A1.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1108
ID ADG34126 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1109
ID ADG62256 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1110
ID ADI81177 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1111
ID ADI33596 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1112
ID ADH69690 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1113
ID ADH25281 standard; protein; 373 AA.
DE Human neurotixin homologue related protein sequence SEQ ID NO:59.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1114
ID ADG09920 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1115
ID ADI15391 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1116
ID ADG09268 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004038335-A1.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1117
ID ADI14723 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1118
ID ADI29851 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1119
ID ADI18318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1120
ID ADM27248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1121
ID ADJ63599 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1122
ID ADJ77494 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1123
ID ADK82842 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1124
ID ADK6606 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1125
ID ADJ65616 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2004038335-A1.
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PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1126
ID ADM27752 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1127
ID ADM17058 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1128
ID ADL06892 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1129
ID ADM42476 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1130
ID ADN05373 standard; protein; 373 AA.
DE Antipsoriatic protein sequence #858.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1131
ID ADM28338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1132
ID ADO36720 standard; protein; 373 AA.
DE Human UKW polypeptide, SEQ ID NO:2.
PN EP1416279-A1.
PD 06-MAY-2004.
PA (HOF ) HOFFMANN LA ROCHE & CO AG F.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1133
ID ADI95820 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1134
ID ADI96372 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207354-A1.
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 1135
ID ADA50171 standard; protein; 412 AA.
DE Human CAR/mouse SCF fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match 7.6%; Score 158.5; DB 6; Length 412;
Best Local Similarity 24.8%; Pred. No. 9.2e-05;
RESULT 1136
ID ADJ67617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 7.5%; Score 157.5; DB 8; Length 351;
Best Local Similarity 23.0%; Pred. No. 8.9e-05;
RESULT 1137
ID ADA50172 standard; protein; 493 AA.
DE Human CAR/mouse anti-CD34 antibody fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match 7.5%; Score 157.5; DB 6; Length 493;
Best Local Similarity 23.7%; Pred. No. 0.00014;
RESULT 1138
ID AAW82729 standard; protein; 264 AA.
DE Adenovirus PACTSG2-SCAR protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 7.5%; Score 156.5; DB 2; Length 264;
Best Local Similarity 25.9%; Pred. No. 7.2e-05;
RESULT 1139
ID AAW82730 standard; protein; 277 AA.
DE Adenovirus SCAR.RGD protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 7.5%; Score 156.5; DB 2; Length 277;
Best Local Similarity 25.9%; Pred. No. 7.7e-05;
RESULT 1140
ID AAU83699 standard; protein; 290 AA.
DE Human PRO protein, Seq ID No 216.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.5%; Score 156.5; DB 5; Length 290;
Best Local Similarity 25.9%; Pred. No. 8.3e-05;
RESULT 1141
ID AAB48145 standard; protein; 373 AA.
DE Human A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.5%; Score 156.5; DB 4; Length 373;
Best Local Similarity 22.2%; Pred. No. 0.00012;
RESULT 1142
ID AAW82731 standard; protein; 397 AA.
DE Adenovirus PACSG2SCAR.sig chimeric protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEEC INC.
Query Match 7.5%; Score 156.5; DB 2; Length 397;
Best Local Similarity 25.9%; Pred. No. 0.00013;
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RESULT 1143
ID ADA50170 standard; protein; 412 AA.
DE Human CAR/SCF fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match
Best Local Similarity 7.5%; Score 156.5; DB 6; Length 412;
Pred. No. 0.00014;
RESULT 1144
ID ABG02019 standard; protein; 737 AA.
DE Novel human diagnostic protein #2010.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.4%; Score 156; DB 4; Length 737;
Pred. No. 0.00035;
RESULT 1145
ID AAB48147 standard; protein; 373 AA.
DE Human A236 variant 3 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.4%; Score 155.5; DB 4; Length 373;
Pred. No. 0.00014;
RESULT 1146
ID ADR66297 standard; protein; 358 AA.
DE Human prostatic carcinoma derived protein SEQ ID 151 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 8; Length 358;
Pred. No. 0.00017;
RESULT 1147
ID ADR66858 standard; protein; 358 AA.
DE Human prostatic carcinoma derived DNA SEQ ID 151 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 8; Length 358;
Pred. No. 0.00017;
RESULT 1148
ID ADA54925 standard; protein; 512 AA.
DE Human protein, SEQ ID 2493.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 6; Length 512;
Pred. No. 0.00028;
RESULT 1149
ID ABP60991 standard; protein; 5635 AA.
DE Novel human protein. SEQ ID 78.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 5; Length 5635;
Pred. No. 0.0086;
RESULT 1150
ID ADJ70089 standard; protein; 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.

PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 7; Length 5636;
Pred. No. 0.0086;
RESULT 1151
ID ADJ83137 standard; protein; 5636 AA.
DE Human hemiscentin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LITX/) LIT X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PAT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LIL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 7; Length 5636;
Pred. No. 0.0086;
RESULT 1152
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 8; Length 5636;
Pred. No. 0.0086;
RESULT 1153
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 8; Length 5636;
Pred. No. 0.0086;
RESULT 1154
ID ADP73129 standard; protein; 5636 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P29.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match
Best Local Similarity 7.4%; Score 154.5; DB 8; Length 5636;
Pred. No. 0.0086;
RESULT 1155
ID AAY53666 standard; protein; 4412 AA.
DE Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608.
PN WO9960164-A1.
PD 25-NOV-1999.
PA (QUAR-) QUARK BIOTECH INC.
Query Match
Best Local Similarity 7.3%; Score 153.5; DB 3; Length 4412;

Best Local Similarity	22.0%;	Pred. No. 0.0074;
RESULT 1156		
ID ADA50158 standard; protein; 393 AA.		
DE Human CAR/mouse SCF mature fusion protein.		
PN US2003092068-A1.		
PD 15-MAY-2003.		
PA (ITOH/) ITOH A.		
PA (HANA/) HANAZONO Y.		
PA (OKAD/) OKADA T.		
PA (OZAW/) OZAWA K.		
Query Match	7.3%;	Score 153; DB 6; Length 393;
Best Local Similarity	24.3%;	Pred. No. 0.00026;
RESULT 1157		
ID ADA50159 standard; protein; 474 AA.		
DE Human CAR/mouse anti-CD34 antibody mature fusion protein.		
PN US2003092068-A1.		
PD 15-MAY-2003.		
PA (ITOH/) ITOH A.		
PA (HANA/) HANAZONO Y.		
PA (OKAD/) OKADA T.		
PA (OZAW/) OZAWA K.		
Query Match	7.2%;	Score 152; DB 6; Length 474;
Best Local Similarity	23.2%;	Pred. No. 0.00041;
RESULT 1158		
ID AAU17996 standard; protein; 301 AA.		
DE Human immunoglobulin polypeptide SEQ ID No 141.		
PN WO200155315-A2.		
PD 02-AUG-2001.		
PA (HUMA-) HUMAN GENOME SCI INC.		
Query Match	7.2%;	Score 151; DB 4; Length 301;
Best Local Similarity	25.8%;	Pred. No. 0.00026;
RESULT 1159		
ID ABB10232 standard; protein; 301 AA.		
DE Human cDNA SEQ ID NO: 540.		
PN WO200154474-A2.		
PD 02-AUG-2001.		
PA (HUMA-) HUMAN GENOME SCI INC.		
Query Match	7.2%;	Score 151; DB 4; Length 301;
Best Local Similarity	25.8%;	Pred. No. 0.00026;
RESULT 1160		
ID ABP66819 standard; protein; 301 AA.		
DE Human polypeptide SEQ ID NO 540.		
PN US2002090672-A1.		
PD 11-JUL-2002.		
PA (ROSE/) ROSEN C A.		
PA (RUBE/) RUBEN S M.		
PA (BARA/) BARASH S C.		
Query Match	7.2%;	Score 151; DB 5; Length 301;
Best Local Similarity	25.8%;	Pred. No. 0.00026;
RESULT 1161		
ID ADB31620 standard; protein; 301 AA.		
DE Human novel protein SEQ ID NO 141.		
PN US2003077606-A1.		
PD 24-APR-2003.		
PA (HUMA-) HUMAN GENOME SCI INC.		
Query Match	7.2%;	Score 151; DB 7; Length 301;
Best Local Similarity	25.8%;	Pred. No. 0.00026;
RESULT 1162		
ID ADR41522 standard; protein; 318 AA.		
DE Human CD-1like molecule HKACT103, SEQ ID NO:321.		
PN WO200226930-A2.		
PD 04-APR-2002.		
PA (HUMA-) HUMAN GENOME SCI INC.		
Query Match	7.2%;	Score 151; DB 5; Length 318;
Best Local Similarity	25.8%;	Pred. No. 0.00028;
RESULT 1163		
ID ADA50157 standard; protein; 393 AA.		
DE Human CAR/SCF mature fusion protein.		
PN US2003092068-A1.		
PD 15-MAY-2003.		
PA (ITOH/) ITOH A.		
PA (HANA/) HANAZONO Y.		
PA (OKAD/) OKADA T.		

PA	(OZAW/) OZAMA K.	
Query Match	7.2%; Score 151; DB 6;	Length 393;
Best Local Similarity	25.4%; Pred. No. 0.00038;	
RESULT 1164		
ID	ABG02117 standard; protein; 434 AA.	
DE	Novel human diagnostic protein #2108.	
PV	WO200175067-A2.	
PD	11-OCT-2001.	
PA	(HYSE-) HYSEQ INC.	
Query Match	7.2%; Score 151; DB 4;	Length 434;
Best Local Similarity	24.3%; Pred. No. 0.00044;	
RESULT 1165		
ID	ABU62399 standard; protein; 466 AA.	
DE	Chimeric CAR/Hg/Pro-A gene product.	
PV	US6524572-B1.	
PD	25-FEB-2003.	
PA	(RAIN-) RAINBOW THERAPEUTIC CO.	
Query Match	7.2%; Score 151; DB 6;	Length 466;
Best Local Similarity	25.4%; Pred. No. 0.00049;	
RESULT 1166		
ID	AAY13563 standard; protein; 1395 AA.	
DE	Drosophila Robo 1 polypeptide.	
PV	WO9925833-A1.	
PD	27-MAY-1999.	
PA	(REGC) UNIV CALIFORNIA.	
Query Match	7.1%; Score 150; DB 2;	Length 1395;
Best Local Similarity	20.5%; Pred. No. 0.0028;	
RESULT 1167		
ID	AAY08401 standard; protein; 1395 AA.	
DE	Drosophila sp. ROBO1 protein.	
PV	WO9920764-A1.	
PD	29-APR-1999.	
PA	(REGC) UNIV CALIFORNIA.	
Query Match	7.1%; Score 150; DB 2;	Length 1395;
Best Local Similarity	20.5%; Pred. No. 0.0028;	
RESULT 1168		
ID	ADB85335 standard; protein; 1395 AA.	
DE	Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1	
PV	US2003170727-A1.	
PD	11-SEP-2003.	
PA	(GOOD/) GOODMAN C S.	
PA	(KIDD/) KIDD T.	
PA	(BROS/) BROSE K.	
PA	(TESS/) TESSIER-LAVIGNE M.	
Query Match	7.1%; Score 150; DB 7;	Length 1395;
Best Local Similarity	20.5%; Pred. No. 0.0028;	
RESULT 1169		
ID	AAB85862 standard; protein; 373 AA.	
DE	Murine adipocytes-derived protein.	
PV	WO200166720-A1.	
PD	13-SEP-2001.	
PA	(KITA/) KITAMURA T.	
PA	(TSUR/) TSURUGA H.	
Query Match	7.1%; Score 149; DB 4;	Length 373;
Best Local Similarity	21.7%; Pred. No. 0.00053;	
RESULT 1170		
ID	ABB68257 standard; protein; 1395 AA.	
DE	Drosophila melanogaster polypeptide SEQ ID NO 31563.	
PV	WO200171042-A2.	
PD	27-SEP-2001.	
PA	(PEKE) PE CORP NY.	
Query Match	7.1%; Score 149; DB 4;	Length 1395;
Best Local Similarity	20.2%; Pred. No. 0.0035;	
RESULT 1171		
ID	AAB48126 standard; protein; 373 AA.	
DE	Mouse A236 polypeptide.	
PV	WO200069885-A2.	
PD	23-NOV-2000.	
PA	(MILL-) MILLENNIUM PHARM INC.	
Query Match	7.1%; Score 148; DB 4;	Length 373;
Best Local Similarity	21.7%; Pred. No. 0.00064;	
RESULT 1172		
ID	AAB26449 standard; protein; 373 AA.	

DE Mouse A236 protein.
PN US2002055139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match 7.1%; Score 148; DB 5; Length 373;
Best Local Similarity 21.7%; Pred. No. 0.00064;
RESULT 1173
ID ABG31321 standard; protein; 2652 AA.
DE Predicted human adican-2 protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 7.0%; Score 147.5; DB 5; Length 2652;
Best Local Similarity 21.8%; Pred. No. 0.012;
RESULT 1174
ID ADL02250 standard; protein; 2652 AA.
DE Human OCP protein #6.
PN US2004053301-A1.
PD 18-MAR-2004;
PA (QUAR-) QUARK BIOTECH INC.
Query Match 7.0%; Score 147.5; DB 8; Length 2652;
Best Local Similarity 21.8%; Pred. No. 0.012;
RESULT 1175
ID ABP70049 standard; protein; 2845 AA.
DE Human NOV1a;
PN WO200272771-A2.
PD 19-SEP-2002;
PA (CURA-) CURAGEN CORP.
Query Match 7.0%; Score 147.5; DB 5; Length 2845;
Best Local Similarity 21.8%; Pred. No. 0.013;
RESULT 1176
ID AAB48149 standard; protein; 373 AA.
DE Mouse A236 variant 2 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000;
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.0%; Score 147; DB 4; Length 373;
Best Local Similarity 21.7%; Pred. No. 0.00078;
RESULT 1177
ID AAB48150 standard; protein; 373 AA.
DE Mouse A236 variant 3 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.0%; Score 147; DB 4; Length 373;
Best Local Similarity 21.3%; Pred. No. 0.00078;
RESULT 1178
ID AAB48148 standard; protein; 373 AA.
DE Mouse A236 variant 1 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.0%; Score 147; DB 4; Length 373;
Best Local Similarity 21.7%; Pred. No. 0.00078;
RESULT 1179
ID ABG22401 standard; protein; 361 AA.
DE Novel human diagnostic protein #22392.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 146.5; DB 4; Length 361;
Best Local Similarity 24.5%; Pred. No. 0.00083;
RESULT 1180
ID ABB66424 standard; protein; 2016 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 26064.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 145.5; DB 4; Length 2016;
Best Local Similarity 22.1%; Pred. No. 0.012;
RESULT 1181
ID ABB64120 standard; protein; 1033 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19152.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 144.5; DB 4; Length 1033;
Best Local Similarity 20.9%; Pred. No. 0.0055;
RESULT 1182
ID ADQ89652 standard; protein; 1033 AA.
DE Antagonist of cell cycle progression polypeptide #41.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 6.9%; Score 144.5; DB 8; Length 1033;
Best Local Similarity 20.9%; Pred. No. 0.0055;
RESULT 1183
ID ADG63213 standard; protein; 367 AA.
DE Human neurotrophin protein +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 144; DB 7; Length 367;
Best Local Similarity 26.6%; Pred. No. 0.0014;
RESULT 1184
ID ADE08316 standard; protein; 538 AA.
DE Novel protein (useful for identifying genetic disorders) #471.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 144; DB 7; Length 538;
Best Local Similarity 20.7%; Pred. No. 0.0024;
RESULT 1185
ID ABB63044 standard; protein; 467 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.8%; Score 143.5; DB 4; Length 467;
Best Local Similarity 22.1%; Pred. No. 0.0022;
RESULT 1186
ID ADE97401 standard; protein; 396 AA.
DE Murine nectin-like protein 1.
PN WO2003064992-A2.
PD 07-AUG-2003.
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR/) LARRICK J W.
PA (WYCO/) WYCOFF K L.
Query Match 6.8%; Score 142.5; DB 7; Length 396;
Best Local Similarity 19.6%; Pred. No. 0.0021;
RESULT 1187
ID AAY69287 standard; protein; 398 AA.
DE Amino acid sequence of long extracellular form of murine B7-1 (CD80).
PN WO200008057-A2.
PD 17-FEB-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 6.8%; Score 142.5; DB 3; Length 398;
Best Local Similarity 19.6%; Pred. No. 0.0021;
RESULT 1188
ID AAE00868 standard; protein; 404 AA.
DE Mouse brain immunoglobulin superfamily receptor (BtGR) protein.
PN WO200129083-A1.
PD 26-APR-2001.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 6.8%; Score 142.5; DB 4; Length 404;
Best Local Similarity 19.6%; Pred. No. 0.0022;
RESULT 1189


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ID ADJ70907 standard; protein; 450 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2713.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
  Query Match      6.8%; Score 142; DB 7; Length 450;
  Best Local Similarity 23.0%; Pred. No. 0.0028;
RESULT 1190
ID ABP70430 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-1 BALB/c allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
  Query Match      6.7%; Score 141.5; DB 6; Length 305;
  Best Local Similarity 24.7%; Pred. No. 0.0018;
RESULT 1191
ID ADE08000 standard; protein; 376 AA.
DE Novel protein (useful for identifying genetic disorders) #155.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
  Query Match      6.7%; Score 141.5; DB 7; Length 376;
  Best Local Similarity 25.2%; Pred. No. 0.0024;
RESULT 1192
ID ADO47897 standard; protein; 463 AA.
DE Mouse protein SEQ ID NO:14.
PN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
  Query Match      6.7%; Score 141.5; DB 8; Length 463;
  Best Local Similarity 21.1%; Pred. No. 0.0032;
RESULT 1193
ID ABO84469 standard; protein; 3475 AA.
DE Human cancer-associated protein HPI3-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match      6.7%; Score 141.5; DB 8; Length 3475;
  Best Local Similarity 27.5%; Pred. No. 0.0057;
RESULT 1194
ID ABB71502 standard; protein; 1052 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41298.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match      6.7%; Score 141; DB 4; Length 1052;
  Best Local Similarity 25.1%; Pred. No. 0.011;
RESULT 1195
ID AAW69698 standard; protein; 352 AA.
DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYNV ) UNIV NEW YORK STATE.
  Query Match      6.7%; Score 140.5; DB 2; Length 352;
  Best Local Similarity 25.4%; Pred. No. 0.0026;
RESULT 1196
ID ABB63920 standard; protein; 359 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
  Query Match      6.7%; Score 140.5; DB 4; Length 359;
  Best Local Similarity 23.0%; Pred. No. 0.0027;
RESULT 1197
ID AAW57213 standard; protein; 376 AA.
DE Mouse coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 19-MAR-1998.
PA (DAND ) DANA FARBER CANCER INST INC.
  Query Match      6.7%; Score 140.5; DB 2; Length 376;
  Best Local Similarity 25.4%; Pred. No. 0.0029;
RESULT 1198

ID ADP56685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL ) LILLY & CO ELI.
  Query Match      6.6%; Score 139.5; DB 8; Length 265;
  Best Local Similarity 24.0%; Pred. No. 0.0021;
RESULT 1199
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN WO200029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
  Query Match      6.6%; Score 139.5; DB 3; Length 310;
  Best Local Similarity 22.0%; Pred. No. 0.0027;
RESULT 1200
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (huJAM3) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (ELIL ) LILLY & CO ELI.
  Query Match      6.6%; Score 139.5; DB 8; Length 310;
  Best Local Similarity 22.0%; Pred. No. 0.0027;
RESULT 1201
ID ADQ8188 standard; protein; 413 AA.
DE Novel human immunosuppressive receptor MCD055 protein sequence SegID2.
PN JP2004208583-A.
PD 29-JUL-2004.
PA (MOCH ) MOCHIDA PHARM CO LTD.
PA (BIOT-) BIOTECHNOLOGY KAIHATSU GIJUTSU KENKYU KU.
  Query Match      6.6%; Score 139.5; DB 8; Length 413;
  Best Local Similarity 23.3%; Pred. No. 0.004;
RESULT 1202
ID AAE23555 standard; protein; 370 AA.
DE Human FAHL protein #4.
PN EP1201681-A1.
PD 02-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
  Query Match      6.6%; Score 139; DB 5; Length 370;
  Best Local Similarity 25.3%; Pred. No. 0.0038;
RESULT 1203
ID ABG72460 standard; protein; 561 AA.
DE Human platelet derived growth factor receptor beta truncation mutant.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
  Query Match      6.6%; Score 139; DB 6; Length 561;
  Best Local Similarity 19.7%; Pred. No. 0.0069;
RESULT 1204
ID ABG20753 standard; protein; 1089 AA.
DE Novel human diagnostic protein #20744.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
  Query Match      6.6%; Score 139; DB 4; Length 1089;
  Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1205
ID ABG72455 standard; protein; 1090 AA.
DE Human platelet derived growth factor receptor beta.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
  Query Match      6.6%; Score 139; DB 6; Length 1090;
  Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1206
ID AAP90127 standard; protein; 1106 AA.
DE Platelet derived growth factor receptor.
PN EP325224-A.
PD 26-JUL-1989.
PA (ZYMO ) ZYMOGENETICS INC.
  Query Match      6.6%; Score 139; DB 1; Length 1106;
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Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1207
ID AAR26205 standard; protein; 1106 AA.
DE Type B human platelet-derived growth factor receptor.
PN WO9213867-A1.
PD 20-AUG-1992.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 6.6%; Score 139; DB 2; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1208
ID AAR99690 standard; protein; 1106 AA.
DE Platelet-derived growth factor receptor.
PN EP721983-A1.
PD 17-JUL-1996.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 6.6%; Score 139; DB 2; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1209
ID ABG72457 standard; protein; 1106 AA.
DE Human platelet derived growth factor receptor beta mutant T672M.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
Query Match 6.6%; Score 139; DB 6; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1210
ID ABG72456 standard; protein; 1106 AA.
DE Human platelet derived growth factor receptor beta mutant E594K.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
Query Match 6.6%; Score 139; DB 6; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1211
ID ABG72459 standard; protein; 1106 AA.
DE Human platelet derived growth factor receptor beta mutant L867M.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
Query Match 6.6%; Score 139; DB 6; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1212
ID ABG72458 standard; protein; 1106 AA.
DE Human platelet derived growth factor receptor beta mutant D826N.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
Query Match 6.6%; Score 139; DB 6; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1213
ID ABP96311 standard; protein; 1106 AA.
DE Human platelet-derived growth factor receptor beta protein.
PN WO2003016540-A2.
PD 27-FEB-2003.
PA (UYYO-) UNIV YORK.
Query Match 6.6%; Score 139; DB 6; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1214
ID ABR84719 standard; protein; 1106 AA.
DE Human PDGF beta receptor protein.
PN WO2003070083-A2.
PD 28-AUG-2003.
PA (CORR) CORNELL RES FOUND INC.
PA (EDEL/) EDELBERG J M.
PA (RAFI/) RAFI S.
PA (HONG/) HONG M K.
PA (LANZ/) LANZA R P.
PA (WEST/) WEST M D.
Query Match 6.6%; Score 139; DB 7; Length 1106;

Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1215
ID ADF45082 standard; protein; 1106 AA.
DE Human kinase PDGFR-b.
PN WO2003081210-A2.
PD 02-OCT-2003.
PA (SUNE-) SUNEIS PHARM INC.
Query Match 6.6%; Score 139; DB 7; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1216
ID ABO84679 standard; protein; 1106 AA.
DE Human cancer-associated protein HP20-018.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 139; DB 8; Length 1106;
Best Local Similarity 19.7%; Pred. No. 0.018;
RESULT 1217
ID AAY96735 standard; protein; 310 AA.
DE PRO1868, an A33 antigen homologue.
PN WO200036102-A2.
PD 22-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1218
ID AAB33457 standard; protein; 310 AA.
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1219
ID AAB27276 standard; protein; 310 AA.
DE Human confuency regulated adhesion molecule 1 #2.
PN WO200053749-A2.
PD 14-SEP-2000.
PA (RMFD-) RMF DICTAGENE SA.
Query Match 6.6%; Score 138.5; DB 3; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1220
ID AAB80272 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1221
ID AAM93905 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 4051.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.6%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1222
ID AAM93323 standard; protein; 310 AA.
DE Human polypeptide, SEQ ID NO: 2845.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.6%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1223
ID AAU12440 standard; protein; 310 AA.
DE Human PRO1868 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 4; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

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RESULT 1224
ID AAB80383 standard; protein; 310 AA.
DE Secreted protein encoded by gene #13.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1225
ID AAB80408 standard; protein; 310 AA.
DE Secreted protein encoded by gene #38.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1226
ID AAB80409 standard; protein; 310 AA.
DE Secreted protein encoded by gene #39.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1227
ID ABG92709 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2002098506-A1.
PD 25-JUL-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1228
ID ABG91361 standard; protein; 310 AA.
DE Novel human secreted protein #7.
PN US2002098505-A1.
PD 25-JUL-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1229
ID ABB84947 standard; protein; 310 AA.
DE Human PRO1868 protein sequence SEQ ID NO:262.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1230
ID ABG65297 standard; protein; 310 AA.
DE Human albumin fusion protein #1972.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1231
ID ABG65296 standard; protein; 310 AA.
DE Human albumin fusion protein #1971.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1232
ID ABG65298 standard; protein; 310 AA.
DE Human albumin fusion protein #1973.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1233
ID ABG31401 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US2002098507-A1.
PD 25-JUL-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1234
ID ABB95553 standard; protein; 310 AA.
DE Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1235
ID ABU71650 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1236
ID ABU72377 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002182618-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1237
ID ABU80867 standard; protein; 310 AA.
DE Human secreted and transmembrane polypeptide PRO1868.
PN US2002192668-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1238
ID ABO17884 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1239
ID ABU71505 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 21.8%; Pred. No. 0.0033; Length 310;
RESULT 1240
ID ADA57610 standard; protein; 310 AA.
DE Human secreted protein #592.
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PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1241
ID ADA57611 standard; protein; 310 AA.
DE Human secreted protein #592.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1242
ID ADA57309 standard; protein; 310 AA.
DE Human secreted protein #592.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1243
ID ABP71277 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (JAM3).
PN WO2003006673-A2.
PD 23-JAN-2003.
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1244
ID ABU81138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003004313-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1245
ID ABU71951 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1246
ID ABO01834 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1247
ID ABU66838 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1248
ID ABU54407 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1249
ID ABO47422 standard; protein; 310 AA.
DE Human secreted/transmembrane polypeptide PRO1868.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1250
ID ABG73314 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US2002164646-A1.
PD 07-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1251
ID ABU59919 standard; protein; 310 AA.
DE Novel secreted and transmembrane protein PRO1868.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1252
ID ABO25109 standard; protein; 310 AA.
DE Human secreted/transmembrane protein (PRO) #269.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1253
ID ABU64559 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #63.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1254
ID ABU67405 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1255
ID ABO14925 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1256
ID ABU60813 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160392-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1257
ID ABU67114 standard; protein; 310 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 538.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1258
ID ABU81236 standard; protein; 310 AA.
DE Human PRO1917polypeptide.
PN US2003032060-A1.
PD 13-FEB-2003.
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Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1277
ID ADA79530 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1278
ID ADA87669 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1279
ID ADB16871 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1280
ID ABO34876 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1281
ID ADA16459 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1282
ID ADA91963 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1283
ID ADB15026 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1284
ID ADB18987 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1285
ID ADA94202 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1286
ID ADB20098 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1287
ID ADB13410 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1288
ID ABO43417 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1289
ID ADA74664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1290
ID ADA42604 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1291
ID ADB24897 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1292
ID ADA82421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1293
ID ADA75384 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1294
ID ADA85462 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1295

ID ADA84910 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1296
ID ABO17554 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1297
ID ADB30166 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1298
ID ADA80694 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1299
ID ADA75936 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1300
ID ADA47161 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1301
ID ADB25457 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1302
ID ADA93633 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1303
ID ADB26983 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1304
ID ADB31270 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1305
ID ABU62957 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003054447-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1306
ID ADA61198 standard; protein; 310 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1307
ID ADB24345 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1308
ID ADA96674 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1309
ID ADA81246 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1310
ID ADA81246 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1311
ID ADA96122 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1312
ID ADB26431 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1313
ID ADB21916 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1314
ID ADA77695 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

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PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1314
ID ADB18435 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1315
ID ADA87118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1316
ID ADA16883 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1317
ID ADA13312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1318
ID ADA42180 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1319
ID ADA88221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1320
ID ADA46609 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1321
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1322
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.
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PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1323
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1324
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1325
ID ABO01894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1326
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1327
ID ADA88773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1328
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1329
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1330
ID ADB22468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
  Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1331
ID ABO17615 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match          6.6%; Score 138.5; DB 7; Length 310;
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Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1332		
ID	ADA67159 standard; protein; 310 AA.	
DE	Human PRO polypeptide #269.	
PN	US2003068793-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1333		
ID	ADB23020 standard; protein; 310 AA.	
DE	Human PRO polypeptide #269.	
PN	US2003077711-A1.	
PD	24-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1334		
ID	ADB23793 standard; protein; 310 AA.	
DE	Human PRO polypeptide SEQ ID NO 538.	
PN	US2003077712-A1.	
PD	24-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1335		
ID	ADA92515 standard; protein; 310 AA.	
DE	Novel human secreted and transmembrane protein PRO1868.	
PN	US2003082712-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1336		
ID	ADB15578 standard; protein; 310 AA.	
DE	Human PRO polypeptide #269.	
PN	US2003087352-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1337		
ID	ADB38830 standard; protein; 310 AA.	
DE	Novel human secreted and transmembrane protein PRO1868.	
PN	US2003082766-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1338		
ID	ADB38278 standard; protein; 310 AA.	
DE	Novel human secreted and transmembrane protein PRO1868.	
PN	US2003087347-A1.	
PD	08-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1339		
ID	ADB66750 standard; protein; 310 AA.	
DE	Novel human secreted and transmembrane protein PRO1868.	
PN	US2003082689-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
RESULT 1340		
ID	ADB89830 standard; protein; 310 AA.	
DE	Human PRO polypeptide #269.	
PN	US2003082698-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	6.6%;	Score 138.5; DB 7; Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;
Best Local Similarity	21.8%;	Pred. No. 0.0033;

RESULT 1341	ID	ADB90562	standard; protein; 310 AA.
	DE	Human PRO polypeptide #269.	
	PN	US2003082762-A1.	
	PD	01-MAY-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1342		
	ID	ADB77948	standard; protein; 310 AA.
	DE	Human secreted/transmembrane protein, #65.	
	PN	US2003077654-A1.	
	PD	24-APR-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1343		
	ID	ADB39663	standard; protein; 310 AA.
	DE	Novel human secreted and transmembrane protein PRO1868.	
	PN	US2003082764-A1.	
	PD	01-MAY-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1344		
	ID	ADB75084	standard; protein; 310 AA.
	DE	Human secreted/transmembrane protein, #65.	
	PN	US2003082542-A1.	
	PD	01-MAY-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1345		
	ID	ADB47286	standard; protein; 310 AA.
	DE	Novel human secreted and transmembrane protein PRO1868.	
	PN	US2003082687-A1.	
	PD	01-MAY-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1346		
	ID	ADB86893	standard; protein; 310 AA.
	DE	Human PRO polypeptide #269.	
	PN	US2003082697-A1.	
	PD	01-MAY-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1347		
	ID	ADB77498	standard; protein; 310 AA.
	DE	Novel human secreted and transmembrane protein PRO1868.	
	PN	US2003082696-A1.	
	PD	01-MAY-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1348		
	ID	ADB34655	standard; protein; 310 AA.
	DE	Human PRO polypeptide SEQ ID NO 538.	
	PN	US2003077717-A1.	
	PD	24-APR-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1349		
	ID	ADB35759	standard; protein; 310 AA.
	DE	Human PRO polypeptide SEQ ID NO 538.	
	PN	US2003077719-A1.	
	PD	24-APR-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1350		
	ID	ADB35759	standard; protein; 310 AA.
	DE	Human PRO polypeptide SEQ ID NO 538.	
	PN	US2003077719-A1.	
	PD	24-APR-2003.	
	PA	(GETH) GENENTECH INC.	
	Query Match	6.6%;	Score 138.5; DB 7; Length 310;
	Best Local Similarity	21.8%;	Pred. No. 0.0033;
	RESULT 1350		


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ID ADB34103 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1351
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1352
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1353
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1354
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1355
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1356
ID ADC40445 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1357
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1358
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1359
ID ADC29624 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1360
ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1361
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1362
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1363
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1364
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1365
ID AAE38826 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1366
ID ADC50579 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1367
ID ADC72126 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1368
ID ADC60105 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
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PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1369
ID ADC53112 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1370
ID ADC57466 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1371
ID ADC60657 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1372
ID ADC51132 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1373
ID ADC65659 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1374
ID ADC54757 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1375
ID ADC53718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1376
ID ADC59241 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1377
ID ADC56119 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087360-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1378
ID ADC58689 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1379
ID ADC12667 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1380
ID ADC74383 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1016.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1381
ID ADC74606 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1239.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1382
ID ADC74607 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1240.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1383
ID ADD03363 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1384
ID ADC90355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1385
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1386
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194773-A1.
PD 16-OCT-2003.

PA	(GETH) GENENTECH INC.	6.6%;	Score 138.5;	DB 7;	Length 310;
Query Match					
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1387					
ID	ADD10192 standard; protein; 310 AA.				
DE	Human PRO polypeptide #269.				
PN	US2003194776-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1388					
ID	ADD04767 standard; protein; 310 AA.				
DE	Novel human secreted and transmembrane protein PRO1868.				
PN	US2003087354-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1389					
ID	ADC80723 standard; protein; 310 AA.				
DE	Novel human secreted and transmembrane protein PRO1868.				
PN	US2003092103-A1.				
PD	15-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1390					
ID	ADD11230 standard; protein; 310 AA.				
DE	Human PRO polypeptide #269.				
PN	US2003194774-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1391					
ID	ADD10551 standard; protein; 310 AA.				
DE	Human secreted/transmembrane PRO polypeptide #131.				
PN	US2003105011-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1392					
ID	ADC48111 standard; protein; 310 AA.				
DE	Human PRO polypeptide #269.				
PN	US2003194771-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1393					
ID	ADD05222 standard; protein; 310 AA.				
DE	Human secreted/transmembrane protein, #65.				
PN	US2003104469-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1394					
ID	ADC80171 standard; protein; 310 AA.				
DE	Novel human secreted and transmembrane protein PRO1868.				
PN	US2003087358-A1.				
PD	08-MAY-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1395					
ID	ADD11511 standard; protein; 310 AA.				
DE	Human secreted/transmembrane PRO polypeptide #131.				
PN	US2003105013-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;			
RESULT 1399					
ID	ADD11511 standard; protein; 310 AA.				
DE	Human secreted/transmembrane PRO polypeptide #131.				
PN	US2003105013-A1.				
PD	05-JUN-2003.				
PA	(GETH) GENENTECH INC.				

Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1396				
ID	ADD09640	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194775-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1397				
ID	ADD04228	standard; protein;	310 AA.	
DE	Human secreted/transmembrane protein, #65.			
PN	US2003104381-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1398				
ID	ADD03804	standard; protein;	310 AA.	
DE	Human secreted/transmembrane protein, #65.			
PN	US2003108983-A1.			
PD	12-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1399				
ID	ADD41353	standard; protein;	310 AA.	
DE	Novel human secreted and transmembrane protein PRO1868.			
PN	US2003203438-A1.			
PD	30-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1400				
ID	ADD52492	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194769-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1401				
ID	ADD53232	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194792-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1402				
ID	ADD53784	standard; protein;	310 AA.	
DE	Novel human secreted and transmembrane protein PRO1868.			
PN	US2003203437-A1.			
PD	30-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1403				
ID	ADD37304	standard; protein;	310 AA.	
DE	Human secreted/transmembrane PRO polypeptide #131.			
PN	US2003105012-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1404				
ID	ADD51940	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194779-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1405				
ID	ADD51940	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194779-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1406				
ID	ADD51940	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194779-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1407				
ID	ADD51940	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194779-A1.			
PD	16-OCT-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	6.6%;	Score 138.5;	DB 7;	Length 310;
Best Local Similarity	21.8%;	Pred. No. 0.0033;		
RESULT 1408				
ID	ADD51940	standard; protein;	310 AA.	
DE	Human PRO polypeptide #269.			
PN	US2003194779-A1.			
PD	16-OCT-2003.			
PA	(GETH			

Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1405
ID ADD02739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1406
ID ADD38106 standard; protein; 310 AA.
DE Human secreted protein #289.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1407
ID ADD38009 standard; protein; 310 AA.
DE Human secreted protein #192.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1408
ID ADD38105 standard; protein; 310 AA.
DE Human secreted protein #288.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1409
ID ADD02173 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1410
ID ADD54355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1411
ID ADD92672 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1412
ID ADD91568 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1413
ID ADE04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1414
ID ADE04182 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1414
ID ADE32479 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1415
ID ADE22411 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1416
ID ADD79635 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1417
ID ADE42171 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1418
ID ADE17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1419
ID ADE17988 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1420
ID ADD92120 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1421
ID ADE34135 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1422
ID ADD80187 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1423
ID ADE34135 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

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ID  ADD93224 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003194768-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1424
ID  ADE19644 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199025-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1425
ID  ADE35056 standard; protein; 310 AA.
DE  Human secreted/transmembrane protein, #65.
PN  US200307583-A1.
PD  24-APR-2003;
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1426
ID  ADE19092 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199028-A1.
PD  23-OCT-2003;
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1427
ID  ADE43288 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199033-A1.
PD  23-OCT-2003;
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1428
ID  ADD96077 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199059-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1429
ID  ADE22963 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199064-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1430
ID  ADD79081 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003203429-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1431
ID  ADE33031 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US2003194766-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1432
ID  ADE42723 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199032-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1433
ID  ADD80739 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003207418-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1434
ID  ADD89767 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199028-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1435
ID  ADE41051 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199031-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1436
ID  ADE04850 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003199034-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1437
ID  ADE92979 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003194777-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1438
ID  ADG21688 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US2003207355-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1439
ID  ADG23329 standard; protein; 310 AA.
DE  Novel human secreted and transmembrane protein PRO1868.
PN  US2003207384-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1440
ID  ADF97664 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
PN  US2003207370-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          6.6%; Score 138.5; DB 7; Length 310;
    Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1441
ID  ADG80728 standard; protein; 310 AA.
DE  Human PRO polypeptide #269.
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PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1442
ID ADG80176 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1443
ID ADH62558 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1444
ID ADH59539 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1445
ID ADH55468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1446
ID ADH56020 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1447
ID ADI38318 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1448
ID ADI64239 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1449
ID ADI65188 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1450
ID ADI63687 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1451
ID ADH82101 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1452
ID ADH81549 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1453
ID ADJ58518 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003170864-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1454
ID ADJ26586 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1455
ID ADM82718 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1456
ID ADN16117 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1457
ID ADN16746 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1458
ID ADN15565 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1459
ID ADI65188 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.


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Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1459
ID ADN15013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1460
ID ADC81275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1461
ID ADE79501 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1462
ID ADD76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1463
ID ADD88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1464
ID ADD86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1465
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1466
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1467
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1468
ID ADE41512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1469
ID ADE23515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1470
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1471
ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1472
ID ADD87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1473
ID ADE89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1474
ID ADE74136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1475
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1476
ID ADE88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1477
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ID ADE9690 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1478
ID ADE94869 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1479
ID ADE91280 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1480
ID ADE95421 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1481
ID ADE93531 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1482
ID ADF35112 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1483
ID ADE98809 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1484
ID ADE92427 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1485
ID ADE90728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1486
ID ADE91875 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1487
ID ADE99236 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1488
ID ADG40706 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1489
ID ADF74100 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1490
ID ADG02454 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1491
ID ADG22240 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1492
ID ADG20310 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1493
ID ADF98216 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1494
ID ADG24433 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207426-A1.
PD 06-NOV-2003.
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PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1495
ID ADF98787 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1496
ID ADG03618 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1497
ID ADF99339 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1498
ID ADG16924 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1499
ID ADG05383 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1500
ID ADG19650 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

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